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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3212); Krammer, P. and Oren, M.

Mueller-Schilling, M.; Krammer, P. and Oren, M.

Mueller-Schilling, M.; Krammer, P. and Oren, M.

Novel receptor dna useful for identifying apoptosis-modulating to the second 
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                                3061 CATGGTGATTTCTGCTTGCTGCTGCTGGTGGTTGGTGGTACTCGTTCCCACCGCACAGA 3120
3181 agaaatgccagcttgcagatggctaatcaaag 32½2
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## В DEFINITION AL157394 ACCESSION REFERENCE SOURCE KEYWORDS COMMENT ORGANISM JOURNAL TITLE AUTHORS FEATURES Direct Submission 2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, W. E-mail enquiries; humquery@sanger.ac.uk Clone requests and the sequence version replaced gi:14161146. CB10 15A, W. E-mail enquiries; humquery@sanger.ac.uk Clone requestssanger.ac.uk replaced gi:14161146. CB10 15A, W. E-mail enquiries; humquery@sanger.ac.uk Clone requestssanger.ac.uk replaced gi:14161146. CB10 15A, W. E-mail enquiries; humquery@sanger.ac.uk Clones. The sequence assembly data is compared from overlapping clones. Note that the puring sequence are found these are anotated as variations. Note that the together with anotation may not be found in the sequence submission and towerlapping clone, as we submit sequences with together with anotation may not be found in the sequence with an alternate only a small overlapping clone, as we submit sequences with regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality programs are problems, such chemistry or covered by high quality data (i.e., phred quality programs are submissed by restriction and sequencing problems, such chemistry or covered by high quality data (i.e., phred quality problems, such chemistry or covered by high quality data (i.e., phred quality problems as compressions and repeats; all regions were covered by at least chemistry or covered by high quality and the gold on the such chemistry or covered by the problems are covered by at least chemistry or covered by the problems are covered by at least chemistry or covered by the problems are covered by at least chemistry are covered by at least chemistry are covered by at least chemistry accession numbers given assembly was confirmed by restriction digest. The following given abbreviations are used to the source databases: Em:, EMBL; Swi. abbreviations are used to the source databases: Em:, EMBL; Swi. substructed to the source databases: Em:, EMBL; Swi. substructed to the source da BASE COUNT ORIGIN Query Match Best Local Similarity source 187313 bp DNA linear PRI 22 AL157394 tuman DNA sequence from clone RP11-399019 on chromosome 10 complete sequence. AL157394 misc\_feature misc\_feature misc\_feature AL157394.15 GI:15384622 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. http://www.sanger.ac.uk/projects/C\_elegans/wormpep This sequence http://www.sanger.ac.uk/project SWISSPROT: Tr. TREMBL; Wp:, WORMPEP; database can be found at \_\_\_\_\_\_ (bases 1 to 187313) http://www.sanger.ac.uk/HGP/Chr10 RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see This sequence is the entire insert of clone RP11-399019 The true requence is the entire insert of clone RP11-496H23 is at 166408 in this sequence. The left end of clone RP11-304I5 is at 18704 in this sequence. true right end of clone RP11-304I5 is at 18704 in this sequence. of Pieter de Jong. For rurcher de htm http://www.chori.org/bacpac/home.htm /organism="Homo sapiens" /db\_xref="taxon:9606" Location /clone="RP11-399019" /clone\_lib="RPCI-11.2" /chromosome="10" /note="Sequence from AC015461 sequenced by WIBR." 105808. 105972 105973. .105989 /note="Sequence confirmed by AC015461 sequenced by WIBR." a 36398 c 36888 g 58358 t /note="Sequence confirmed by AC015461 sequenced by WIBR." 100157. .100198 note="Sequence from AC015461 sequenced by WIBR." 99.2%; 99.7%; score 3185; pred. No. 0; DB 9; Length 187313; PRI 22-AUG-2001

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Db 142989 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA 143048
                                   Db 142929 Greatgeaaageceteaggaaggtaacetaacetagatttgagggeceaaacaggeteca 142988
                                                                       Db 142869 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 142928
                                                                                                           Db 142809 GGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 142868
                                                                                                                                               Qy 781 taccatccttatcccacttcttttgtgtctattagatgctcagagtgtgtgcacaa 840
Db 142749 TACCATCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA 142808
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                                               961 gtgatggaaagccctcaggagggtaacctaacctagatttgagggccc-aacaggctcca 1019
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Oy 1000 ttaatgtgttattaatgggttgaatctaabb 143049 TMANTGTGTTATTAATGGGTTGAATGATAATGGGTTGAATGATAATGGGTTGAATGATAATGGGTTGAATGATAATGGGTTGAATGATAATGAGTTGAATGAATGAATGAAAAAA		
THATTHAATGGTTGAATCHA TATTTAATGGTTGAATCTA TATTTAATGGTTGAATCTA TATTTAATGGTTGAATCTA TATTTAATGGTTGAATCTA TATTTAATGGTTGAATCTA TATTTAATGGTTGAATCTA TATTCAGGTTCAGTAATGAT TACCCCAAAGGAT TACCCCAAAGGATTACACCC TACCCCTAAAGAATTACAATCTAAATCTAAAAAATTACAAATTACAAATTACAAAAAA	Db 143529 GTCTGTGAC  Qy 1620 tettetet  Db 143589 TCTTTCTCTY  QY 1680 gctetgaget  Db 143649 GCTCTGAGGT  QY 1740 gcctttagaa  Db 143709 GCCTTTAGAA  QY 1800 cactgcaggaa  Db 143769 CACTGCAGGAA  QY 1800 tcaccctgact  Db 143769 CACTGCAGGAA  QY 1860 tcaccctgact  Db 143829 TCACCCTGAGGAA  QY 1920 cctcccaaccc  Db 143889 CTTCCCAACCCT  QY 1920 cttcgcaaccc  Db 143889 CTTCCCTAACCC  Y 1980 ttttgtgagct  Db 143949 TTTTCGTGAGCTC  Y 2040 ctgggagagagagagagagagagagagagagagagagaga	OY 100 ttaatgt
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Db 144189 AACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTGAGCCCTCTCCTGCCCGGGTG 144248
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                                     3120 aacccggcgcctattattggccaagaaacttgagcagcctgttttgaaaagtccctcgct 3179
            3180 cagaaatgccagcttgcagatggctaatcaaag 3212
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                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                       421 actaaccatotttgccaatgttgcttaagcttttttggctacatttttttatttgtaaag 480
                                                                            2827 bp
Sequence 4 from Patent DE19847779.
AX026092
541 cacatatgtgagttgctggcttataattcacactcaagagatactgattttgtcaattgt 600
                                     541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
Novel receptor dna useful for cancer chemotherapy
substances potentially useful for cancer chemotherapy
patent: DE 19847779-C 4 03-FEB-2000;
patent: REDESFORSCH (DE)
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1. 2827
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676 c 657 g
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Oy 2820 ggttaagccggagggcto	2760 a 2368 A	Oy 2700 cgggtgggtgagtgcgcc		Qy 2580 acaggaattgaagcggs	Qy 2520 gcagctccggcgctcc	Qy 2460 atggaggacttgcttt Db 2210	QY 2400 gttggagactggctc	Qy         2340 gggattgcggcggca           Db         2210	Oy 2280 gaggettaccccgto Db 2188	Db 2188	22 2	2 2 2	•	OY 1980 ttttcgtgagcto	•		Oy 1800 cactgcaggaa 	<del>-</del>	i i

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                                                                                        misc_signal
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                                                         enhancer
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                                                                                                                                                                                                                                                                                                                                       2344 bp DNA H. Sapiens CD95 gene 5' flanking region., x87625
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2344)

Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
                                                                                                                                                                                                                                                                                                                        beta interferon; CD95 gene; silencer.
                                                                                                                                                                                                                                                                                                                                 x87625.1 GI:902311
                                                                                                                                                                       96069539
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                                  /note="beta interferon silencer B motifs"
complement(1237. .1244)
complement(1237. .1244)
/note="lysozyme silencer 1"|
1388. .1919
1338. .1919
1920. .2344
/note="basal promoter"
a 546 c 511 g 650 t
                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                           /chromosome="10"
                                                                                                                   /tissue_type="placenta"
/map="q24.1"
                                                                                                   /note="silencer"
                                                                                                                                     germline
        68.9%;
         Score 2211.8; DB 9;
              Length 2344;
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Matches 2224; Conservative 0; Mismatches
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                          0; Mismatches
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TGATGGAAAGCCCTCAwwards
961 9494-994-994-994-994-994-994-994-994-99
1018 ACAAGCCTATCAAAAGCCTAGAATTTTTTTTTTTTTTTT
GGCACTAACAGTCTA
ACCATCCTCCTTATCCCACTTCTTTTTTTCTCACCACCAC
781 tacca
GATA
78 CTTCCCTCACACCCCTTTTTTTTTTTTTTTTTTTTTTT
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718 CCTTTCCCCTTTTTTCTCTCTCTCCTCCTCCTTCCTTC
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ACATATGTGAGTTGCTGGCT1A1AAA
Oy 541 cacatatgtgagttgctggcttataatlCacacacacacacacacacacacacacacacacacacac
81 taagtttaataat
538 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCT
478 AAGAGCAGCATCTTTTTTTTTTTTTTTTTTTTTTTTTTT
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Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University,
Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa,
Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp,
Te1:076-234-4424, Fax:076-234-4480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakanishi, y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection. Chem. 270 (30), 18007-18012 (1995)
Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    66.7%; Score 2143.4; 99.7%; Pred. No. 0;
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2100 gcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctcttctcccgc 2159 2158 CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGCACTG

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1860 tcaccctgacttctccccctccctacccgcgcgcgcaggccaagttgctgaatcaatggagc 1919

1918 CACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCCTGACTCCTTCC 1977

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                                   481 GTGGTAAGTGCAGTGACAGATGCAAAACACAGGGTGATGGAAAGCCCCTCAGGAGGGGTAAC 540
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AUTHORS
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Best Local Similarity 84.9%; Score 1899.6; DB 6; Length 2380;
Matches 2348; Conservative 0; Mismatches 24; Indels 394; Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2380)
Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating patent: DE 1984779-C 3 03-FEB-2000; Cancer chemotherapy
DEUTSCHES KEBSEFORSCH (DE)
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Tocation (Maria II films)
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/label=Hsmxv-1" /product="APO-1" /product="APO-1" /1689. 1810 /gene=APT" /gene=APT" /label=ex1c /label=1 /number=1 /usedin=x81335:HsmRNA3 /usedin=x81336.1:155320,x81337.1:146. /mRNA /join(17041810,x81336.1:155320,x81337.1:146.	mrna X81338.1:145253254255279.x0139263263279279263263279.	exon /gene="APT" /label=exla /number=1 /number=1 /number=1 /number=1 /number=1 /number=1 /number=1 /gene="APT" /gene="APT" /label=exlb /number=1 /	/label-HsmRNAH. /label-HsmRNAH. /product="APO-1"   1810, x81336.1:155320, x81337.1:146. /product="1810, x81336.1:155828, x81340.1:79. /oin(165318131:155253, x81339.1:552828, x81340.1:79. /gene x8138.1:145279, x81342.1:1031757) /gene="APT" /gene="APT" /gene="AP	ich region" 1336.1:155. X81339.1:552 (81341.1:255.	JOURNAL Center, pumorimulo 1091 75  Center, page 100 / Qualifiers  FEATURES	1 (bases 1 Behrmann, I Behrmann, I Behrmann, I Structure Eur. J. Im 95104292 95104292 2 (bases Krammer, P Direct Su Direct Su	TION ION NDS RDS	1368 T

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927 ggtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaa 986
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X81340.1:79 .161,X81341.1:255. .279,X81342.1:103. .1757)
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ORIGIN

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Matches 1874;

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                                                                                              Query Match 47.8%; Score 1536.8; Best Local Similarity 98.6%; Pred. No. 0; Matches 1582; Conservative 0; Mismatches
                                                                                                                                                                                                 exon
                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                      source
                                                H.sapiens Fas, Apo-1 gene (promoter and exon I). x82279
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1608)
Cheng,J., Liu,C., Koopman,W.J. and Mountz,J.D. Characterization of human Fas gene. Exon/intron organization and Characterization of human Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X82279.1 GI:673405
                                                                                                                                                                                                                                                                                                                          Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham, Of Alabama, 701 South 19th Street, UAB Station, LHRB 473, Univ. of Alabama, 701 South 19th Street, UAB Station, LHRB 473, Birmingham, AL 35294-0007, USA Related sequences: M67454 and X63717.
                                                                                                                                                                                                                                                                                                                                                                                                                 promoter region
J. Immunol. 154 (3), 1239-1245 (1995)
95123075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APO-1 gene; FAS gene.
                                                                                                                                                                                                                                                                                                                                                                              Cheng,J.
Direct Submission
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                                                                                                                                                                              /gene="Fas, Apo-1"
1075. .1496
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421 c 423 g
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1075, 1496
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b 1086 CCCTGACTCCTTCCCCCAacccgg y 1906 tgaatcaatggagccctccccaacccgg	ы ю <u>с</u>
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1726 gaactacagcagaagcotttagaaagggcaggaggcggctgtcgaaggtccuckers, 1726 gaactacagcagaagccotttagaaagggcaggaggcggctgtlllllllllllllll	, KO
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7 atgcaanaccagggtgatggaagccctcaggagggtaacctaacc	D
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1422 АТАСААААСАСААЛАТААТААААААСССТСААЛАААТААССТААССТААСТТАААТТТАААЛАС 1363
                                                  ORGANISM
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            947 atgcaaaacacagggtgatggaaagccctcaggaggggtaacctaacctagatttgagggc 1006
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1 51 c 421 g 770 t
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                       343 ATTCAAAAACGCTTCTAAAAAATAAAAAAAACGATTTACGAATAACTTAACTAAAACCTC 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1002 ААССААЛАЛАТААТАААТААССААЛААЛААСАЛАЛААТТАТАЛАТАТТТААТАТААСТАА 943
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2218 tcaaccatgctgggcatctggaccctccttagtgatcctctggtgatccctctctggtgatccctctgttgt	1398 GCGGGTTGGTTGGTTAGTACGGAGTTGGGGAAGTTIIIIIIIIII	2158 gogggttggtggaccogotcagtacggagttggggaagototttoacttoggaggactvv - 2158 gogggttggtggaccogotcagtacggagttgggagtgg	2098 tggcacgaacacccccgagyccusyccist		2038 ttctggggagtgagggaagcggtttacgagtgacttggctggagcctcagggggggg	1978 gcttttcgtgagctcgtctctgatctcgcgcaagagtgacacacagggggtccaaagacyc 200 	TAATTCGGGCGTTTTTTAGCGAGGTTTTTTTTTTTTTTT	090 IIIIAAIIIAAAAAAAAAAAAAAAAAAAAAAAAAAA	858 cctcacctgacttctcccccctacccgcgcgcgugucuagreyccgiiiiiiiii		8 gccactgcaggaacgcccgggacaggaatgcccatttgtgcaacgaaccctgactcctt 185	38 aagcetttagaaagggeaggaggegggcteggagytettettestest   1   1   1   1   1   1   1   1   1	GAGTTTTATTTTTTTTTTTAAGATTTTTTTTAATTTTTTT	g gcgctctgagctccattctccttccaggacctcccccaacttcccaggttgaactacagcay - /	GTATTTAGGTAGGATTTTT 91	CGTTTGTGAGTTTTTATGTTGTAGTTATAAGATGGATAGTTAGTAG	58 acgtctgtgagcctctcatgttgcagccacaacatggacagcccagtcaaatgccccycu vo	TGTTTATTTTAGGA	679 TGGTTTAAGIIGIAGACACAACATCTTCTCACACATATGGTTAACCTGTCCAGTCCAG	38 tggcttaagttgttagctttgttttcctcttgagaaataadaccaayyycciii 138 tggcttaagttgttagctttgttttcctctttgagaaataadaccaayyycciii 138 tggcttaagttgttgttgtgtgtgtgtgtgtgtgtgtgtg		78 atgagtaacgaagg	A 61	99 TTTATGTTAAATTATTTAAGAGATTACAGAGATTATTTAT	58 ttcatgctaaactacctaagagctatctaccgttccaaagcaatagtgacttcyaccy		98 aactgcatccaaattcaggttcagtaatgatgtcattatccaaacataccttctgtaaaa 12	ø

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Direct Submission
Submitted (19-SEP-2000) Muschen M., Department of Immunology,
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                           Related sequences: D31968 X89101 AJ279011 AJ279013
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Kuppers, R. and Rajewsky, K.
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1 (bases 1 to 702)
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                                                     /product="CD95 antigen"
/protein_id="CAC35540.1"
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/standard_name="Apo-1 Fas
                /gene="CD95"
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282. .>313
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                              2006 cgcaagagtgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacg 2065
                                                                                                                                                                        2126 ctggctgcccaggcggagctgcctcttctcccgcgggtttggtggacccgctcagtacgga 2185
2246 tcctacctctggtgatccctctcctgcccgggtggaggcttaccccgtcttagtcccggg 2305
                                          181 CTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCGGGTTGGTGGACCCGCTCAGTACGGA
                                                                                                                                                         121 AGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGGCACGGAACACCCTGAGGCCAGCC 180
                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 702)
Muschen, M., Re, D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R., and Rajewsky, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                 CGCAAGAGTGACACAGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACG
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/note="Hodgkin's disease tissue"
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pred. No. 9.1e-152;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                               Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                                                                                                  Related sequences: D31968 x89101 AJ279011 AJ279012
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V., Kuppers,R. and Rajewsky,K.
Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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Muschen L. C. 702)
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                                           /standard_name="Apo-1 Fas"
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                                                                                                                                                                                                                                                                                              Location/Qualifiers
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LOCUS BC012479 2719 bp mRNA linear PRI DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor
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                                                                                                                                                                        601 CTGCGCTCCACGTTGAGGTGGGCATGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGA
                                                                                                                              2606 agctttagggtcgctggagggggaccccggfttggagagagga 2647
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                                                                                                         661 AGCTTTAGGGTCGCTGGAGGGGGGACCCCGGTTGGAGAGAGGA 702
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198 c
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REFERENCE

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ORGANISM

Homo sapiens

DEFINITION HSA2.79013 Š В δÃ B δĀ В

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/number=1 /gene="CD95"

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JOURNAL

Direct Submission Muschen, M. Unpublished

AUTHORS JOURNAL TITLE

AUTHORS

(bases 1 to 702)

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                                                                     1977 ggcttttcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacg 2036
                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-Aug-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2719)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: i Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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RCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLT
SNTKCKEEGSBSNLGWLCLLLLPIPLIYWVKRKEVQKTCRKHRKENQGSHESPTLNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           superfamily, member 6"
/protein_id="AAH12479.1"
/db_xref="GI:15214692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_"MGC:21432 IMAGE:4514272†
/tlssue_type="Bladder, transitional cell papilloma"
/clone_lib="NIH_MGC_93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                TVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Similar to tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                            LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV/
                                                                                                                                                                      10.6%; Score 342; DB 9; Length 2719;
100.0%; Pred. No. 7.1e-69;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  532 c
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Search completed: September 7, 2002, 18:21:38 Job time: 28797 sec

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
                                                                                                                                                                          Result
                                                                                                                                                           NO.
                                                                                                                                                                                                                                         pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            1536.8
                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     September 7, 2002, 10:21:46; Search time 1139.19 Seconds (without alignments) 4840.921 Million cell updates/sec
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3212
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                      1: \side \text{SIDSI}\gcgdata/\nold-geneseq/geneseqn-embl/\NA1981.DAT: *
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19: \side \text{SIDSI}\gcgdata/\nold-geneseq-geneseqn-embl/\NA2000.DAT: *
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Listing first 45 summaries
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                                                                                                                                                             Match Length DB
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 1608
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2471
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16
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ABL34418
                                    AAC61798
AAQ93879
                                                                     AAC98177
AAZ88700
                                                                                                                                     AAT34162
     AAQ29959
                                                                                                                                                                                                                        SUMMARIES
                                               Human colon cancer
Human CD95 recepto
DNA encoding a hum
Fas-delta-TM CDNA.
                                                                                                                                                                                  Description
                                                                                                                                                  Fas promoter regio
                                                                                                                     Human
                  Human cell surface
                                 Soluble Fas recept
                                                                                                                     immune syste
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                                  RESULT
AAT34162
AAT34167
AC AAT
XX AAT
XX 22-
XX Pas
KW Pas
KW T-C
XX Fas
KW T-C
YY KC
FT Pr
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1.7 21537

1.6 16033

1.6 162450

1.6 12138

1.6 15484

1.6 8622

1.6 8899

1.6 11960

1.6 399

1.6 399
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35100
38258
8888
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38886
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5893
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AAT16303
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AAZ23892
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                                                                                                                                                     ABL32500
AA185367
                                                                                                                                                                                                                                                       AAT34529
                                                                                                                                                                          ABL34572
                                                                                                                                              AAA96417
                                                               ABL33629
                                                                       AAZ86967
                                                      AAK70808
                                                                                                                                                                                                                                                                                                                                 Human Fas antigen
                                                                                                                                                                                                                                                                                                                                           Fas cDNA.
                                                                                                                                                                                                                                                           Human colon cancer
Human Fas soluble
Human Fas soluble
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EP-892047 Seq ID 4
                                                                                                                                                                                                                                                                                                                Human c-fms oncoge
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Murine LOBO genomi
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Nucleotide sequenc
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            Human nervous syst
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                                                                                                             immune syste
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## ALIGNMENTS

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RESULT 1

AART34162

XX

XX

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XX

AART34162;

XX

XX

XX

Fas gene promoter region.

XX

XX

Fas gene promoter; apoptosis; ageing; autoimmune disease;

XX

XX

YAS

Homo sapiens.

XX

XX

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YAS

Homo sapiens.

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YAS

Homo sapiens.

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YAS

Homo sapiens.

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Homo sapiens.

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Homo sapiens.

YAS

Homo sapiens.

XX

Homo sapiens.

YAS

Homo sapiens.

YAS

Homo sapiens.

AN

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

FT

Protein_bind 147..151

YAS

Homo sapiens.

Location/Qualifiers

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

YAS

Homo sapiens.

Location/Qualifiers

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

YAS

Homo sapiens.

Location/Qualifiers

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

YAS

Homo sapiens.

Location/Qualifiers

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

YAS

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

YAS

Homote "Fas gene promoter region"

FT

Protein_bind 147..151

Homote "Fas gene promoter region"

FT

Protein_bind 148..174

And The Homote Promoter Promoter
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Matches 1582;
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                                                                                                                           A novel DNA segment (AAT34162) has an isolated sequence region defined as the Fas gene promoter region. This includes a number of transcription factor binding sites. A coding sequence for its also included. The DNA segment was isolated from leader peptide corresponding to nt 23-346. It can be combined with a structural gene so that the gene is under the transcriptional control of the transcription factor binding sites. The promoter region can be used a means of treating Fas-mediated apoptosis disorders such as
827 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 886
                   Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;
                                                                                                                                                                                                                                                   Claim 11; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                    Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas mediated
                                                                                      Local
                                                                                                                                                                                                                                                                                                               P-PSDB; AAR99471.
                                                                                                                                                                                                                                                                                                                                      Cheng J, Koopman WJ,
                                                                                                                                                                                                                                                                                                                                                        (UABR-) UAB RES FOUND.
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                                                                                  Similarity
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          96WO-US00606.
                                                                            47.88;
98.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= Fas protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function= CP2 transcription factor binding site
/note= "claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function= Ap-1 transcriptio factor binding site
/note= "claim 5"
1037..1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function= NF-Y transcription factor binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= GF-1 transcription factor binding site
/note=_"claim 7"
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                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                Score 1536.8;
Pred. No. 0;
0; Mismatches
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"5' end of intron 1 (full length approx.
14 kb"
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                                                                                                                                                                                                                     907 ggcaggacctctgcgctctgagctccattctccttcaagacctccccaacttcccaggtt 966
                                                                                                                                                                                                                                                                                            1606 aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca 1665
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                                                                                                                                                                                                                                                                           847 aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca 906
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03-JAN-2002.

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| 2086 agggggggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagct 1385
| 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 1111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 11| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 11| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 111| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarteriosclerotic; antianaemic; cytostatic; nontropic; antiarteriosclerotic; antiarteriosculanti-navi antionvulsant; ophthalmological; neuroprotective; anti-HTV; antidabetic; antipsoriatic; anaemia; neuroprotective; canti-ntitic; antidabetic; antipsoriatic; anti-neumatic; antiarthritic; antidabetic; antipsoriatic; anti-neumatic; antiarthritic; eye disease; arteriosclerosis; anaemia; antiinflammatory; cancer; eye disease; alibs; epilepsy; antiinflammatory; cancer; alzheimer's disease; alibs; epilepsy; ancute myeloid leukaemia; alzheimer's disease; alibs; epilepsy; acute myeloid leukaemia; alzheimer's disease; alibs; acute myeloid leukaemia; alzheimer's disease; alibs; acute myeloid leukaemia; alameimia; al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                          WO200200928-A2.
                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                     30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG.
                                     Nucleic acid comprising fragment of chemically modified gene, useful nucleic acid comprising fragment of diseases associated with abnormal for diagnosis and treatment of diseases associated with abnormal cytosine methylation
Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
                                                                                                                                                                                                        Berlin K;
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76.6%;
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762 AAATACCCCGCAAATCTTTCTCTAAATAACTCCAACAATTAACCAAAACTCCTATACCCA 703

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RESULT
Human; immune system disease; cytosine methylation, antiasthmatic; antiarteriosclerotic; antianemic; cytostatic; nootropic; anti-Hry, anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsordatic; acute myeloid leukaemia; Alzheimer's disease; arteriosclerosis; anaemia; alzheimer's disease; Alzs; epilepsy; anaemia; alzheimer's disease; properties anaemia; alzheimer's disease; arteriosclerosis; anaemia; alzheimer's disease; alzheimer's disease; alzheimer's disease; alzheimer's disease; anaemia; alzheimer's disease; alzheimer's disease; anaemia; alzheimer's disease; alzheimer's disease; alzheimer's disease; alzheimer's disease; alzheimer's disease; alzheimer's disease; anaemia; alzheimer's disease; alzheimer
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                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                        δĀ
                                                                                                                                                                                                                                                                                              B
            1258 ttcatgotaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagt 1317
                                                                                                                                                                                                                                                                                                                γ
                                                                                                                                                                                                                                                                                                                                    В
499 tttatgttaaattatttaagagttatttatcgttttaaagtaatagtgattttgaatagt 558
                                                  1198 aactgcatccaaattcaggttcagtaatgatgtcattatccaaacataccttctgtaaaa 1257
                                                                                                                                                                                                                                                                                                                                                     δĀ
                                                                                                                                                                                                                                                                                                                                                                            B
                                        439 aattytatttaaatttaggtittagtaatgatgitattatttaaatatatttittgiaaaa 498
                                                                                          1138 gtgcagaggttggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctgg 1197
                                                                              379 gtgtagagtttggtggacgatgttaaaggaatattgaaattittagtgtgtttagtttgg 438
                                                                                                                                1078 tattaatgtgttattaatgggttgaatctaattgggaagggagagagggttgcagagtgag 1137
                                                                                                                     319 tattaatgtyttattaatgggttgaatttaattgggaagggagagaggttgtagagtgag 378
                                                                                                                                                                        1018 cagaagaaatgtcaactgagaggaagcctgaaggatgaacagtgggctaagcaaagggt 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 tagaagaaaatgitaattgagaggaagttigaaggatgaatagtgggttaagtaaagggt 318
                                                                                                                                                                                                                                                                                                                                                                                               Matches 1215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                    959 999tgatggaaagccctcaggagggtaacctaacctagatttgaggg-cccaacaggctc 1017
                                                                                                                                                                                                                                           139 agataagtttattaatatttataagattggtggtaagtgtagtgatagatgtaaaatata 198
                                                                                                                                                                                                                                                        899 agacaagcotatcaacacctacaagactggtggtaagtgcagtgacagatgcaaaacaca 958
                                                                                                                                                                                                                                                                                                839 aaggetggeaegeecagggtetteeteatggeaetaacagtetaetgaaaggtggaacag 898
                                                                                                                                                                                                                                                                                   79 aaggitggtacgtttagggtttttttttatggtattaatagtttattgaaaggtggaatag 138
                                                                                                                                                                                                                                                                                                                                      779 tataccatcotcottatoccacttotttttgtgtctattagatgctcagagtgtgtgcac 838
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of human immune system associated can be used in the diagnosis and treatment of fumune system associated including eye diseases such as retinopathy, neovascular glaucoma and leukaemia, Alzheimer's disease, ANDS, epidesy, neurofibromatosis and diseases. The present sequences of arthritis, psoriasis and infilammatory, neurofibromatosis, diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                      h
Similarity 29.8%; Score 957.4; DB 24; Length 1608;
15; Conservative 0; Mismatches 371; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1498 ttcagagccttatggcgcaacatctgtactttttcatatggttaactgtccattccagaa 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1618 agtotttototgagtgactocagcaattagccaaggctoctgtacccaggcaggacctot 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1738 aagcetttagaaagggcaggaggceggetetegaggteeteacetgaagtgageatgeea 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799 acgittgigagittitttatgitgiagitataagatggatagittagittagatgittcgia 858
                                                                                                                                                                                                                                                                                                                                                                                               1038 gttattgtaggaacgtttcgggataggaatgtttatttgtgtaacgaattttgattttt 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        919
                                                                                                                                                                                                                                                                                                                                                                 1858 cctcaccctgacttctccccctccctacccgcgcgcaggccaagttgctgaatcaatgga 1917
                                                                                                                                                                                                                                                                           1978 gcttttcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacgc 2037
                                                                                                                                                                                                                                                                1218 gtttttcgtgagttcgtttttgatttcgcgtaagagtgatatataggtgtttaaagacgt 1277
                                                                                                                                                                                                                               1338
                                                                                                                                   1398
                                                                                                  2218 tcaaccaaccatgctgggcatctggaccctcctacctctggtgatccctctcctgcccggg 2277
                                                                                                                                                        2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atgagtaacgaaggataggaagtaattgtgaatgtitaatatagttggggttatgcgatt 678
1575 gcgggattgcggcggtacggcgtatcgcggg 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acytotytyaycototoatyttycaycoacaacatyyacaycocaytcaaatycocogca 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttagagttitatggcgtaatatttgtattttttatatggttaatttgtttattttagga 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcgctctgagctccattctccttcaagacctccccaacttcccaggttgaactacagcag 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agtttttttttgagtgattttagtaattagttaaggtttttgtatttaggtaggattttt 918
                                                                                                                                                                                                                                                                                                                                                                                                           gccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaaccctgactcctt 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                           aagttittagaaagggtaggaggtcggttttcgaggttittatttgaagtgag-atgtta 1037
                                                                                                                                                                                                                                                                                                            ttttattttgattttttttttttttttttogcgcgtaggttaägttgttgaattaatgga 1157
                                                                                                                                                                                                                      gcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggaggattgc 2217
                                                                                                                                                                          gcgggttggtggattcgtttagtacggagttggggaagtttttttatttcggaggattgt 1457
                                                                                                                                                                                        tggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctcttctccc 2157
                                                      tggaggcttaccccgtcttagtcccggggataggcaaagtggggcggggcgcgggacgcgt 2337
                                                                                       ttaataattaigtigggtattiggattittiattitiggigagtittitittigticggg
                                           gcgggattgcggcggcagcggggcacgcgggg 2368
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RESULT
AAC98177
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                                   γ
밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                        Query Match
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification; cytostatic; cardioactive; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200055351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The treatment and diagnosis of colon disorders, such as colon cancer. The proventides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune may also be used to prevent diseases such as neural disorders, immune system disorders muscular disorders, reproductive disorders, infectious gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB94007 represent sequences used in the exemplification of the present sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB53420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular, human colon cancer antigens can have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective, immunomodulatory, gynaecological, gastrointestinal, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, a vulnerary, nephrotropic, antiinfective and antibacterial polynucleotides, can be used in gene therapy. The colon cancer antigen polynucleotides, can be used in gene therapy. The colon cancer antigen polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                              Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                           1954 cttcccatcctcctgaccaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 2013
                                                                                                                                                                                                                                                                                      invention.
                  2014 tgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacgagtgactt 2073
                                                                              19
                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer; colon cancer antigen; diagnosis; detection;
                                                                        cgtccgcccacgcgtccgaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 78
tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 138
                                                                                                                                                           294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0124270.
                                                                                                                                                                                    96.4%;
                                                                                                                                                                                                     8.9%;
                                                                                                                                                                                    Score 287.4; DB
Pred. No. 1.5e-67
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                           DB 21; Length 859;
                                                                                                                                                                                Indels
                                                                                                                                                                                    0;
                                                                                                                                                                                    Gaps
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0

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Matches 264;
                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAZ88700
           2500 gatcccgctgggcaggcggggcagctccgggcgctcctcgggagaccactgcgctccacgtt 2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis modulating substances potentially useful for canneer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γQ
                                                                                                        Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                               region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                            Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                        Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
                                                                                                                                                                                                                                                                       WPI; 2000-162245/15.
                                                                            Local
                                                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
1 gatcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                          16-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                          DE19847779-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ88700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ88700 standard; DNA; 266 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2194 agetettteaetteggaggattgeteaaceaaceatgetgggeatetggaceeteetacet 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2254 ctggt 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2074 ggctggagcctcagggggcggggcactggcacggaacacccctgaggccagccctggctgc 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 agctctttcacttcggaggattgctcaaccaaccatgctgggcatctggaccctcctacct 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 ctggt 323
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccaggoggagctgcctcttctcccgcgggttggtggacccgctcagtacggagttgggga 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99ctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccctggctgc 198
                                                           Conservative
                                                                                                                                                                                                                                                                                       Mueller-Schilling M,
                                                                                                                                                                                                                                                                                                                                      98DE-1047779.
                                                                                                                                                                                                                                                                                                                                                          98DE-1047779.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 160..179
                                                                   99.28;
                                                                                                                                                                                                                                                                                                                                                                                                                        bound_moiety= p53
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                  8.2%;
                                                          0;
                                                                 Score 262.8;
Pred. No. 3.5
                                                  Mismatches
                                                                                                                                                                                                                                                                                       Oren M;
                                                               3.5e-61;
                                                                   _ DB_21; Length 266;
                                                    ب
                                               Indels
                                                                                                                                  a p53 binding
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В

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The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5' untranslated region, translational start site, translational termination region of 3' untranslated region of nucleic acid molecules encoding Fas, Fas phosphatase). The antisense compounds are used to inhibit the expression of Fas, Fast or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC61798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                     Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                             Example 2; Page 71-73; 116pp; English.
                                                                                                                                                                                                                                              P-PSDB; AAB19341.
                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                  10-APR-2000; 2000WO-US09540
                                                                                                                                                                                                                                                                                                                                12-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                              19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                     WO200061150-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas associated protein 1; protein tyrosine phosphatase; autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC61798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC61798 standard; DNA; 2551 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2740 gagcctacagccttcagaacacatat 2765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2620 tggagggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaa 2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 gagcctgcagccttcagaacagatat 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2560 gaggtgggggggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 tggaggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaa 180
                                                                                                                                                                                                                                                        2000-628395/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9a99t999c9t99999g9g9acaggaattgaagcggaagtctgggaagctitagggtcgc 120
                                                                                                                                                                                                                                                                              Marcusson EG;
                                                                                                                                                                                                                                                                                                                          99US-0290640.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
221..1228
                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
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Matches 252; Query Match

7.8%; Score 252; DB 21; Length 2551; Local Similarity 100.0%; Pred. No. 1.2e-57; Local Similarity 0; Mismatches 0; Indels 0; les 252; Conservative 0; Mismatches 0; Indels 0;

indels 0;

Gaps

0;

2067 gtgacttggctggagcctcaggggcgggcactggcacggaacacacctgaggccagccc 2126

61 gtgacttggctggagcctcaggggcggggcactggcacggaacacaccctgaggccagccc 120

2127 tggctgcccaggcggagctgcctcttctcccgcgggttggtggacccgctcagtacggag 2186

tggctgcccaggcggagctgcctcttctcccgcgggttggtggacccgctcagtacggag 180

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멍 Š

2247 cctacctctggt 2258

cctacctctggt 252

AAQ93879;

06-NOV-1995 (first entry)

Fas-delta-TM cDNA.

Fas-delta-TM; transmembrane deletion; apoptosis; antibody;

adoptive immunotherapy; transgenic animal; ss.

Homo sapiens.

Location/Qualifiers

AAQ93879 standard; cDNA; 2471 BP.

7

W09513701-A. 26-MAY-1995

15-NOV-1994;

94WO-US13173.

93US-0152443.

15-NOV-1993;

(LXRB-) LXR BIOTECHNOLOGY INC.

Barr PJ, Kiefer MC,

Shapiro JP;

p-pSDB; AAR76238. WPI; 1995-200120/26.

mRNA was obtd. from human lymphocytes and PCR was used to make CDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the

Claim 3; Fig.3-1 to 3-4; 38pp; English.

mat\_peptide sig\_peptide

/\*tag= b 243..1136

195..242 195..1139 /\*tag=

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New nucleic acid encoding Fas protein without/its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
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AAX24878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX24878 standard; DNA; 2471 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 7.0%; Score 226; Di
Local Similarity 100.0%; Pred. No. 1.4
es 226; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Fas receptor; Fas ligand; Fast; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble Fas receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX24878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
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CDS
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                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                           polyA_signal
                                                                                                                                                    28-JAN-1999.
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                                                                                                                              16-JUL-1998;
                                                          Chen J, Nabel GJ;
                                                                                 (UNMI ) UNIV MICHIGAN
                                                                                                       17-JUL-1997;
Inhibition of proinflammatory responses - using an agent which
                        P-PSDB; AAW98070
                                     WPI; 1999-132243/11.
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                            97US-0052829
                                                                                                                                  98WO-US14771.
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195..242
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243..1136
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2455..2460
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2349..2354
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AAQ29959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC (see AAW98070). The invention provides a method for inhibiting a colimunosuppressive agent which inhibits the proinflammatory response in a cell mixture by administering an CC immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (Fasi). In some embodiments, Fasi is coadministered comparison to the immunosuppressive agent, and the cell mixture comprises completely inhibit endogenous embodiments, Fasi is coadministered compressive agent, and the cell mixture comprises completely inhibit endogenous pressive agents include antisense completely inhibit endogenous Fasi egents include antisense considered that inhibit endogenous Fasi egents that inhibit endogenous Fasi egents that induce the compressive agents that induce the compressive agents that induce the compressive agents that induce the compressive agent such as completely expression of transforming growth factor (TGF)-beta. The method can be used for treating diseases associated completely expenses host disease, or an autoimmune disease such as completely expenses agent such as completely expense to the complete expense of the comple
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                                                                                                      conflict
                                                                                                                                                                          mat_peptide
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Best Local :
                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                  Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 226;
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  Human cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ29959 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ29959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 attgctcaacaaccatgctgggcatctggaccctcctacctctggt 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2033 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 2092
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Local Similarity 100.0%; Pred. No. ...
Conservative 0; Mismatches
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                                                                                                                                                       /*tag= a
243..1199
/*tag- c
/note- "this residue is not present in pF3"
                                                                                                 /product= Fas_antigen
||046
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 226; DB 20; Length 2471; Pred. No. 1.4e-50;
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RESULT 10
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Plasmid pF58 contg. human Fas cDNA.
                               19-FEB-1996 (first entry)
                                                                  AAQ95297;
                                                                                 AAQ95297 standard; cDNA; 2534 BP.
                                                                                                                                                        2213 attgctcaaccaaccatgctgggcatctggaccotcctacctctggt 2258
                                                                                                                                                                                                      2153 otcocgoggsttggtggacccgotcagtacggagttgggggagctcttcacttcggagg 2212
                                                                                                                                         181 attgctcaacaaccatgctgggcatctggaccctcctacctctggt 226
                                                                                                                                                                                                                                                           2093 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The cDNA was ligated to BstXI-cut vector pcEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey coscatis which were then suspended in buffer containing murine anti-Pas attibodies. The Fas expressing cells adhered with goat anti-mouse extrachromosomal DNA was prepared from adhered to the plates. Extrachromosomal DNA was prepared from adhered to the plates and used to consitive clone (pF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORF corresp. (i.e. human Fas antigen).
                                                                                                                                                                                       121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
                                                                                                                                                                                                                                                                                                                2033 gacgcttctgggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                            61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
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                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monocional antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itoh N, Nagata S, Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR28084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1991;
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Similarity 100.0%; Pred. No. ...
Careervative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92EP-0107060.
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2352..2357
/*tag= e
2518..2523
                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 226; DB 13; 100.0%; Pred. No. 1.5e-50;
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f
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Length 2534;
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antibody production; diseases; treatment; prevention; ds. Plasmid pF58; human Fas cDNA; soluble membrane protein;

Homo sapiens

Location/Qualifiers

mat\_peptide sig\_peptide

/\*tag= b 243..1199 /\*tag= c /\*tag= 195..2

.242

JP07115988-A 09-MAY-1995.

26-OCT-1993; 26-OCT-1993;

> 93JP-0267644. 93JP-0267644

(NISB ) JAPAN TOBACCO INC.

P-PSDB; AAR78606

WPI; 1995-202847/27.

Preparation of soluble membrane proteins  $\cdot$  for their use in antibody production for the treatment and prevention of related diseases

Example 1; Pages 15-17; 51pp; Japanese.

AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins the prodn be used in antibody prodn. for the treatment and prevention of can be used in antibody prodn. for the treatment and prevention of

Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

related diseases.

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SXXCCCCCCCCCCXX SXX PT PT XXX PA XXX PX XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0uery Match 7.0%; Score 226; DB 17; Length 2534; Best Local Similarity 100.0%; Pred. No. 1.5e-50; Matches 226; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the coding sequence for the human Fas antigen contained within the plasmid pCEV4/DFas. The soluble Fas antigen is included in the immunoassay kit of the invention. The kit is for the included in the immunoassay kit of the invention. The kit is for the say of soluble Fas antigen and contains an immobilised anti-soluble Fas assay is standard soluble Fas antigen encoded monoclonal antibody, as well as the standard soluble Fas antigen encoded by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hachiya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systemic lupus erythematosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 49-52; 124pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
                                                                                                                                                                                                                                                                               2093 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152
                                                                                                                                                          2153 otocogoggttggtggaccogctcagtacggagttggggaagctctttcacttcggagg 2212
                                  121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg
181 attgctcaaccaaccatgctgggcatctggaccctcctacctctggt 226
                                                                                                                                                                                                                                                    61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                   1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996-087635/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Noguchi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94JP-0154706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-JP00349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
195..242
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195..1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
243..1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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XXEXEX
XXXXX
                                                                                                                      RESULT 11
                                                                                             AAT16303 standard; cDNA; 2534 BP
Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
                      hFas coding sequence from plasmid pCEV4/hFas.
                                               06-SEP-1996
                                                  (first entry)
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AAV32993

RESULT

12

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Query Match Best Local 9 Matches

7.0%; Score 226; DB 16; Length 2534; Local Similarity 100.0%; Pred. No. 1.5e-50; Local Similarity 0, Mismatches 0; Indels 0; les 226; Conservative 0; Mismatches 0; Indels 0;

0;

Gaps

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2093 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152

0;

61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120

2153 ctcccgcgggttggtggacccgctcagtacggagttgggggaagctctttcacttcggagg 2212

ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180

2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092

1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60

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AAV32993 standard; cDNA; 2534 BP.

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CC depletion of the invention. The method is concerned with reducing CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK) Cells in an immune cell population which also comprises of Fas-igand CC immune cell population which also comprises of Fas-igand CC immune cell population with an effective amount of an agent (e.g. a cc identifying suitable agents which can reduce depletion of activated CC is soluble Fas-Fc fusion protein) which would interfere with the cg. a cc identifying suitable agents which can reduce depletion of activated CC fas-expressing CD8+ TK cells in immune cell populations. Also claimed CC is the use of the agent in the manufacture of therapeutic compositions. CC cell surface receptor Fas and its ligand Fast. By interaction of the cc and its interaction, the method described and its preparations can prevent CC apoptosis of CD8+ TK lymphocytes caused by expression of Fast on activated CD4+ cells. Such Fast-expressing activated CD4+ cells of CD4+ cell infection with an immunodeficiency virus (STV). The claimed prevention of apoptosis may then allow cc treatment (prophylactic and/or therapeutic) of immunodeficiency virus (GTI) activity contained contained prevention of apoptosis may then allow treatment (prophylactic and/or therapeutic) of immunodeficiency.
Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 10; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-456867/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW49104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screaton GR, Xu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL; CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV; simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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/*tag= c
1831..1836
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243..1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Fas protein"
195..242
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RESULT
The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region fr the amino-terminal to (but excluding) the 1st cysteine residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                 Disclosure; Fig 1-2; 102pp; Japanese.
                                                                                            Fas antigen derivative containing modified extracellular region - has low antigenicity, promotes apoptosis and is useful in treatment
                                                                                                                                                P-PSDB; AAW50289.
                                                                                                                                                       WPI; 1997-558981/51.
                                                                                                                                                                              Nagata S, Nakamura N;
                                                                                                                                                                                                               (MOCH ) MOCHIDA PHARM CO LTD
                                                                                                                                                                                                                                          02-MAY-1996;
                                                                                                                                                                                                                                                                  01-MAY-1997;
                                                                                                                                                                                                    (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               W09742319-A1.
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                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Fas antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV07002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV07002 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2213 attyctcaaccaaccatgctgggcatctggaccctcctacctctggt 2258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcagggggg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226;
                                                                                                                                                                                                                                       96JP-0135760.
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243..1199
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                                                                                                                                                                                                                                                                                                                             /product= Fas_antigen
                                                                                                                                                                                                                                                                                                                                                                                                     195..1202
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100.0%; Pred. No. 1.5e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2534;
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RESULT 14
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XX AAF688
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XX Human;
KW Lung C
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Best Local S
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The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, of the coding DNA in gene therapy) to particular viral diseases e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lung tumour protein related nucleotide sequence SEQ ID NO:796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-1999;
15-OCT-1999;
17-DEC-1999;
30-DEC-1999;
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                                                                                                                                                                                                                                                                            06-MAR 2000; 200005-0519642.
22-MAR 2000; 2000US-0533077.
27-MAR 2000; 2000US-0546259.
27-MAR 2000; 2000US-0566406.
05-JUN-2000; 2000US-0589184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gacgcttctggggagtcagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
Lung tumor-associated proteins and the nucleic lacids that encode them, useful for preventing, diagnosing and treating lung cancer -
                                                                                     WPI; 2001-071488/08.
                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
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99US-0419356
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99.6%;
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                                                                                                                                                                                Fanger GR,
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                                                                                                                                                                                            Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                     Carter D;
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CC associated proteins (I) and the nucleic acids (NAS) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC (inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC diagnosis of diseases py rectifying mutations or deletions in a patient's genome
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the production of (I). Additionally, the
CC NAS may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC and complementary sequences may also be used as DNA probes in diagnostic
CC and complementary sequences may also be used as DNA probes in diagnostic
CC and sasays to detect and quantitate the presence of similar NA sequences in
CC assimilar NA sequences in need of treatment for lung
camples, and hence which patients may be in need of treatment for lung
camples, and activity of the protein. AAF68083 to AAF68878 and
CC AAB76848 to AAB76878 represent human lung tumour protein related
CC of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 415-416; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2435 BP; 620 A; 599 C; 614 G; 601 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2374 TAGATTTACAGAGAAGTTGCAGAGAGAGAGAAAGAGTTCCTGTATACCCTTCACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV20441 standard; DNA; 35100 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 ttttccttccttctttttacatttttttatttaaatgaacttttcattttqqaatagttt 735
                                                                                                                                                                                                                                                                                                                          Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisense oligonucleotide; c-fms; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV20441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           736 taggatttcaaaaaatttgcagagataatacagagaatgcccatataccatcctcc 791
                                                                                                                                                                                                                                                                                                                                                                                       Human c-fms oncogene.
                                                                                                                                                                                                                                                           US5734039-A.
                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                          31-MAR-1998
                                                                                                                                                 15-SEP-1994;
                                                                                                                                                                                    15-SEP-1994;
Anticancer composition comprising two anti-sense oligo:nucleotide(s)
                                     WPI; 1998-229882/20.
                                                                          Calabretta B,
                                                                                                            (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                Skorski T;
                                                                                                                                                     94US-0306691
                                                                                                                                                                                        94US-0306691.
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 Mismatches

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Pred. No. 2.1e-05;
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Search completed: September 7, 2002, 18:39:36 Job time: 29870 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.9%; Score 59.8; DB 19; Length 35100; Best Local Similarity 55.6%; Pred. No. 0.00012; Matches 115; Conservative 0; Mismatches 92; Indels 0;
                                                                                  3986 ttctttcttttttctatctttttgaga 4012
                                                                                                                                           The present sequence represents an oncogene from the present invention. The present invention describes a composition which comprises two cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, C-yes. The second oligonucleotide is specific for a proto-oncogene selected from ras, raf, EGF-1, proto-oncogene selected from proto-oncogene or proto-oncogene or proto-oncogene or proto-oncogene or proto-oncogene or proto-oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, C-rel, c-vav, c-ski, c-spi, cyclin Dl, pML/RAR alpha , AMLL/MTGB, The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
                                                                                                                                                                                                                                                                                 3806 gaggttgcagtgagctgagatcatgccactgcactccagcctaggcgacagagcaagact 3865
                                                                                                         714 acttttcattttggaatagttttagga 740
                                                                                                                                                              Sequence 35100 BP; 8474 A; 8597 C; 9682 G; 8347 T; 0 other;
                                                                                                                                                                                                                                                                                                      534 gaagatccacatatgtgagttgctggcttataattcacactcaagagatactgattttgt 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 59-90; 92pp; English.

    targetting cytoplasmic and nuclear oncogene(s)

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В δĀ

C 1 125 100.0 617 9 AV655647  C 2 125 100.0 619 9 AV655647  C 3 125 100.0 899 9 10 BE569266  C 4 123.4 98.7 599 10 BE763679  C 5 121.8 97.4 793 10 BI763679  C 6 110.8 88.6 1140 10 BG121070  C 6 110.8 87.2 35.9 9 AV69383  C 7 109 87.2 36.9 9 AV69383  C 10 87.2 39.1 9 AA383161  9 62.4 49.9 29.1 9 AA383161  10 37 29.6 850 10 BE745387  C 11 36.6 29.3 33.9 AI623104  C 12 36.6 29.3 426 10 BE908413  14 36.6 29.3 426 10 BE908413  15 36.6 29.3 427 10 BE910359  C 15 36.6 29.3 437 9 AW299892  C 17 36.6 29.3 437 9 AW299892	: EST:*  1: em_estba:*  2: em_esthum:*  3: em_esthu:*  4: em_esthu:*  4: em_estcw:*  6: em_estcv:*  7: em_estcv:*  8: em_htc:*  10: gb_est1:*  11: gb_htc:*  11: gb_htc:*  12: pb_gss:\nu:*  13: em_gss_hum:*  14: em_gss_pun:*  15: em_gss_pun:*  16: em_gss_vvr:*  16: em_gss_vri:*  17: em_gss_vii:*  18: em_gss_vii:*  19: gb_est2:*  11: gb_htc:*  11: gb_htc:*  12: pb_gss:\nu:*  13: em_gss_hum:*  14: em_gss_lum:*  15: em_gss_lum:*  16: em_gss_vii:*  16: em_gss_vii:*  Soore greater than or equal to the score of the total score	Gencore version 4.5  search, using sw model  search, using sw model  tember 7, 2002, 14:51:33; S  tembe
AV695647 AV695047  AV695647 AV695047  B17630709 AL540709  BF569266 602185634  B1763679 603349567  B121070 603352793  AV692383 AV692383  B1463384 503204413  AA383161 EST96716  BE745387 601578024  A1633104 tu49f10.x  A1933907 ty905609.x  A1933907 ty905609.x  A1933907 ty905609.x  A1933907 ty905609.x  A1939397 x854602.x  AW299539 x854602.x  AW299539 x854602.x	RESULT 1 BG659530/c LOCUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS ORGANISM He result being printed, distribution.  Description  Description  REFERENCE AUTHORS  TITLE JOURNAL COMMENT  BG659530 TgESTzya2	me 8462.63 Seconds  c 29 c 21 c 22 c 23 c 24 c 25 lignments) lion cell updates/sec c 28 c 29 c 31 c 31 c 33 c 34 c 34 27472414  c 43 c 43 c 44 c 45
rel: 314 286 1810  Fax: 314 286 1810  Email: toxo@watson.wustl.edu  Contact David Sibley (toxoest@borcim.wustl.edu) for further  Contact David Sibley (toxoest@borcim.wustl.edu) for further  Contact David Sibley (toxoest@borcim.wustl.edu) for further  Contact David Sibley (toxoest@borcim.wustl.edu) for clone availability.  Seq primer: -40RP from Gibco  Seq primer:	BG659530 TGESTZYAZ4901.Y1 TGVEGII CDNA CIONE TGESTZYAZ4901 ALPHA-SMOOTH MUSCLE ACT. BG659530.1 GI:13801991 EST. Toxoplasma gondii. Toxoplasma gondii. Toxoplasma fondii. Tang,K., Cole,R., Foyar Clifton,S., Pape,D., Ma Hillier,L., Kucaba,T., ,E., Maguire,L., Waters Toxoplasma EST project Unpublished (2001) Contact: Clifton,S. Contact: Clifton,S. Toxoplasma EST project	36.6 29.3 441 10 BG057358 AIG12753 tp44a01.x 36.6 29.3 459 AIG12753 AIG12753 tp44a01.x 36.6 29.3 464 9 AIG57020 36.6 29.3 476 19 AIG57020 36.6 29.3 476 10 BG236320 AIG75768 AIG657020 oy75a06.x 36.6 29.3 476 10 BG236320 AIG7586 AIG

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FEATURES
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                                                                                                                                                                       Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                   Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                            Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                               Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AV695647 GKC Homo sapiens cDNA clone GKCFCD11 5', mRNA sequence.
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                                                                                                                                                                                                                              86-21-50801919(ex.45)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2;
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/Clone="GKCFCD11"
                                                                               /clone_lib="GKC"
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a small percentage contaminants from human fibroblast
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61 gaggtgggggtggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL540709 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE002YN18 5 prime
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1 (bases 1 to 899)
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                                                                                                                                                                                                                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and encibed, double-stranded cDNA was digested with Not I pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, contact is peng Liang Life Technologies, a waryland 20850, USA Fax: (1) 301 610 8371 Email: http://cilifetech.com/URL:
                                                                                                                                                                                                                http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                              /clone="CSODE002YN18"
/clone_lib="LTI_FL002_PL1"
                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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CDNA Library Arrayed by: The I.M.A.G.E. consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.!

PAR Sequencing by: Incyte Genomics, Inc.!

Clone distribution: MGC clone distribution information can be close distribution: MGC clone of through the I.M.A.G.E. Consortium/LLNL at: found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov

Plate: LLCM1184 row: column: 10

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Linehan
                                                                                                           TGGAG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4909757
/clone_tib="NIH_MGC_45"
/clone_tib="NIH_MGC_45"
/tissue_type="renal carcinoma (ascites)"
/tissue_type="renal carcinoma (ascites)"
/tissue_type="renal carcinoma (processes)"
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into EcoRI/XhoI sites using the following 5 adaptor:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               98.7%; Score 123.4;
99.2%; Pred. No. 2.5
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557 GACCCCGCTGGGCAGGCGGGGCAGCTCCGGGCGCTCCGGAGACCACTGCGCTCCACGTT 498
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BI763679
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BI763679 MRNA Linear EST 25-SEP-2001
603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
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1 (bases 1 to 793)

NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue procurement: Life Technologies, Inc.
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Plate: LLAM11474 row: e column: 17
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                                                BG121070 1140 bp mRNA linear EST 30-04
602352793F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451039
BG121070.1 GI:12614579
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/clone_lib="NIH_MGC_116"
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Homo sapiens

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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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High quality sequence stop: 727.
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Tissue Procurement: ATCC
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/lab.host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pcMV-SPORT6; Site_1: NotI;
Site_1: Sall; Cloned unidirectionally; Oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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/clone_lib="NIH_MGC_90"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.6%; Score 110.8; DB 1
97.6%; Pred. No. 2.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GAGGTGGGCGTGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                      Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
http://lmage.llnl.gov
Plate: LLAM11681 row: j column: 03
                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI463384.1 GI:15254040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603204413F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5270114 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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                                /clone="IMAGE:5270114"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="organ: testis; Vector: pBluescriptR (modified
                                                                        /db_xref="taxon:9606"
                                                                                         /organism="Homo sapiens"
                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             __note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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/dev_stage="hdult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="GKC"
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                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Robert C. L. Allana, C. L. Gocayne, J.D. White Adams, M.D., Kerlavage, A.R., Flieschman, T.L., Geoghagen, N.S., Glodek, A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald Cline, T.R., Cotton, M.D., Earle-Hughes, J.J., Geoghagen, N.S., Glodek, A., L.M., Fitzhugh, W.C., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Merrick, J.M., Shirley, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Phillips, C.A., Ryder, S.E., Coleman, T.A., Collins, E.J., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hu, W.J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Hu, Shirley, F., Ferrie, A., Fischer, C., Hunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weiter, J.C., Wing, J., Fannon Wei, Y.F., Ming, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P. J., Fannon Wei, Y.F., Margan, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C., Traiteil ascerement of human can diversity and avvascerion matterns.
                   source
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AA383161
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence hatter 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, Mp 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                        Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi/html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                              Seq primer: M13 Reverse
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98.5%;
/organism="Homo sapiens"
                                                           Location/Qualifiers
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Pred. No. 2.5e-05;
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BASE COUNT
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BE745387
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Minamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Nath. Botheria; Primates; Catarrhini; Hominidae; Homo.
Nath. MgC http://mgc.nci.nih.gov/.
Nath. MgC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BE745387
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM755 row: p column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLCM755 row: p column: 06 High quality sequence stop: 722.
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/db_xref="taxon:9606"
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                                                                                                     /note="Organ ovary Vector: POTB7; Site_1: XhoI; Site_2: /note="Organ ovary Vector: POTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally EcoRI; cDNA made by oligo-dT priming. Directionally closed states using the following 5. Cloned into EcoRIXhoI sites using the following 5. Size-selected >500bp for average adaptor: GGCACGAG(G). Size-selected by Ling Hong in insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CNNA synthesis kit California, Berkeley) using TAP-CNNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:3927029"
/clone_lib="NIH_MGC_9"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_nost="DH10B (phage-resistant)"
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pred. No. 3.6e-05;
Score 37; pB 10; Length 850; pred. No. 35;
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Local Similarity

64;

Conservative

Mismatches

Indels

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29.6%; 58.7%;

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                     63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Consortium/Claudian Control Consortium/Claudian Cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 321 POLYA=NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the circles were made in vitro. Following HAP purification, reaction. The driver was PCR-amplified cDNAs from a pof 5,000 clones made from the same library (cloneIDs 98508-986759, 1101192-1101959, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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/clone="IMAGE:2254411"
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58.98;
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Pred. No. 37;
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AI393907/c
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171 GGTGGGGGGGGTGTCCGGTCCGGAAATGAAGGAATAGCCCGAGGACC 125
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                                                                                                                                                       63 ggtgggcgtgggggggggacaggaattgaagcggaagtctgggaagc 109
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BE908413
426 bp mRNA linear EST ZU-UCI-Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Clous M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Content of Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 746 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI393907

tg05f09.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107913 3',
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128 c 101 g 71 t
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/clone="IMAGE:2107913"
/clone_1ib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                      Score 36.6;
Pred. No. 38;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGGGGGCGGGTGTCCGGAAATGAAGGAATAGCCCGAGGACC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9711 row: o column: 09 High quality sequence stop: 420. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
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                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)
                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BE910359
                                                                                                                                                                                                                                                                                               BE910359.1 GI:10406871
                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                               Unpublished (1999)
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) by Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: pancreas; Vector: pCMV-sporm6; Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life Technologies."
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plate: LLAM9711 row: p column: 07
High quality sequence stop: 426.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Allzadeh, John Byrd, M.D., Mike Grever,
                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
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/note="organ: pancreas; vector: pCMV-SPORT6; Site_1: Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life rechnologies."
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/note=Tvector: pT7T3D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
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                                                                                                                   /db_xref="taxon:9606"
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Search completed: September 7, 2002, 14:51:36 Job time: 16195 sec

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Result
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Query
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1 (bases 1 to 266)

1 (bases 1 to 266)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 1944779-C 32 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
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Sequence 32 from Patent DE19847779.
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                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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AD002483 Oryza sat
AC104581 Homo sapi
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AC105644 Rattus no
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Mueller,M., Wilder,S., Bannasch,D., Israeli,D., Lehlbach,K.,
Li-Weber,M., Friedman,S.L., Galle,P.R., Stremmel,W., Oren,M. and
                                                                                                                                                                                                                                                                                                                                                                                             99059827
                                                                                                                                                                                                                                                                                                                                                                                                     p53 activates the CD95 (APO-1/Fas) gene in response to DNA damage by anticancer drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Homo sapiens DNA for enhancer of CD95 gene, partial
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72 c 110 g
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159. .178
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159. .178
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Submitted (19-SEP-2000) Muschen M., Department of Immunology,
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Related sequences: D31968 X89101 AJ279011 AJ279013.
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Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
Kuppers,R. and Rajewsky,K.
Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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                                                                                                                        Conservative
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282. .>313
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 720)

1 (bases 1 to 720)

Mueller-Schilling, M., Krammer, P. and Oren, M.

1 (bases 1 to 720)

Mueller-Schilling, M., Krammer, P. and Oren, M.

1 (bases 1 to 720)

Novel receptor day useful for cancer chemotherapy

Novel receptor day useful for cancer chemotherapy

Substances Potentially useful for cancer chemotherapy

Substances Potentially useful for cancer chemotherapy

Patent: DE 1944779-C 2 03-FEB-2000;

Patent: DE 1944779-C 2 73-FEB-2000;

Patent: DE 1946779-C 2 73-FEB-2000;
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Sequence 2 from Patent DE19847779.
AX026090
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h 100.0%; Pred. No. 1.1e-18;
Similarity 100.0%; Pred. No. 0; Mismatches 0;
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Sequence 1 from Patent DE19847779.
                                                                      Novel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy substances potentially novel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy patent: DE 19847779-C 1 03-FEB-2000; patent: DE 19847779-C 1 03-FEB-2000;
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
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/db_x181 c 216 g 181
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HSA279011
Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
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Ruschen, M. Re, D. Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Muschen, M., Rajewsky, K., Kuppers, R. and Rajewsky, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-SEP-2000) Muschen M., Department of Immunology, 50931 Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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/gene="CD95"

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 GACCCCGCTGGGCAGGCGGGCAGCTCCGGGGGGCTCCTCGGAGACCACTGCGCTCCACGTT 614
                                                                                                                                                                   Related sequences: D31968 x89101 AJ279011 AJ279012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 gaggtgggcgtgggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 120
                                                                                                                                                                                        Direct Submission
Submitted (19-SEP-2000) Muschen M., Department of Immunology,
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gatcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                       Muschen, M.
                                                                                                                                                                                                                                                              Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                     (bases 1 to 702)

Muschen M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,

Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                        Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction
                                                                                                                                                                                                                                                                                                                                                    Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (Dases 1 to 702)
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             AJ279013.1 GI:13539242
Apo-1 Fas; CD95 antigen; CD95 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSA279013
Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSA279013
/standard_name="Apo-1 Fas"
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                   /gene="CD95"
                                /standard_name="Apo-1 Fas"
282. .>313
                                                /gene="CD95"
                                                                     /standard_name="Apo-1 Fas"
                                                                                       /gene="CD95"
                                                                                                       /cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue-polymorphic allele (+337)"
                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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98.48;
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FEATURES COMMENT

CDS 5'UTR

exon

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REFERENCE

AUTHORS JOURNAL TITLE

TITLE

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CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone During sequence assembly data is compared from overlapping clones wariation annotation may not be found in the sequence wersion replaced as variations only a small overlap as described above. Note that the This sequence was finished as follows unless otherwise noted: all as compared from overlapping clone name. Note that the Chemistry or covered by high quality data (i.e., phred quality > a stempt was made to resolve all sequencing problems, such abbreviations and repeats; all regions were covered by at least the one plasmid subclone or more than one MI3 subclone; and the sasembly was confirmed by restriction digest. The following surspansions are used to associate primary accession numbers given the feature table with their source databases: Em: EMBL; Sw:, http://www.sanger.ac.uk/Protente/
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10, Further information can be found at RPII-399019 is from the library RPCI-11, 2 constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 GÁGGTGGGCATGGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGGTCGC 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA sequence from clone RP11-399019 on chromosome 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="CD95 antigen"
/protein_id="CAC35541.1"
/db_xref="GI:13539243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLGIWTLLPLV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121.8; DB 9;
Pred. No. 5.7e-18;
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                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The left end of clone RP11-30415 is at 18704 in this sequence true right end of clone RP11-30415 is at 18704 in this sequence. 1. 187313
protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
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h
Similarity 98.4%; pred. No. 2.2e-18;
Similarity 98.4%; pred. No. 2.2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA for Fas antigen, promoter region.
                                                                                                                                                                                                                                                                                                                                                                                        D31968.1 GI:961455
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens blood DNA, clone pF7.
                                                                                                                                                                                                                                                                                  Wada,N., Matsumura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2165)
                                                                                                     Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Tel:076-334-4424, Fax:076-234-4480)
                                                                                                                                                                                                                       factor for interleukin-6 expression upon influenza virus infection J. Biol. Chem. 270 (30), 18007-18012 (1995)
                                                                                                                                                                                                                                                      Transcription stimulation of the Fas-encoding gene by nuclear
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/note="Sequence from AC015461 sequenced by WIBR."
105973. .105989 /note="Sequence confirmed by AC015461 sequenced by WIBR."
26398 c 36888 g 58358 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="sequence confirmed by AC015461 sequenced by WIBR." 100157 ... 100198
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        /tissue_type="blood" 79. .87
                                     /clone="pF7'
                                                    /db_xref="taxon:9606"
                                                                /organism="Homo sapiens"
                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                          misc_RNA
                                                                                                                                                              30urce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 bp DNA linear ptN 16-MAY-2001 phoebe formosana 185 ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5,85 ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 265 ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                             Chanderbali, A.S., van der Werff, H. and Renner, S.S.

Phylogeny and historical blogeography of Lauraceae: evidence from the chloroplast and nuclear genomes the chloroplast and nuclear genomes ann. Mo. Bot. Gard. 88 (1), 104-134 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Phoebe.
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                                                                                                                                                                                                                                                                                                            2 (bases 1 to 733)
Chanderball, A.S., van der Werff, H. and Renner, S.S.
                                                                                                                                                                                                                            Submitted (26 MAY-2000) Biology, University of Missouri-St. Louis, St. Louis, Missouri 63121, USA 8001 Natural Bridge Rd. St. Louis, Missouri 63121, USA
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276. .:
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1814. >2165
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/protein_id="BAA20850.1"
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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 26S ribosomal RNA"
                                                       /note="contains 18S ribosomal RNA, internal transcribed
                                                                                                                                                 /organism="Phoebe formosana"
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                                                                                                                 /db_xref="taxon:128687"
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BASE COUNT

138 a

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DEFINITION Sequence 2726 from Patent W00194629
                                           AX332217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolation of a cDNA which corrects chromosome breakage in Fanconi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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377 c
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                                                                                                                                                                                                                                                           /product-"DNA repair protein"
/product-"DNA repair protein"
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                                                                                                                                                                                                                                                                                                                                                   /Standard_name="51C protein"
/function="corrects chromosome breakage in Fanconi anemia
                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="immortalized fibroblast"
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                                                                                                                                                                                     29.3%;
58.9%;
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ll_line="GM 639"
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PAT 09-JAN-2002
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Hejna, J.A., Saito, H., Merkens, L.S., Tittle, T.V., Jakobs, P.M., Whitney, M.A., Grompe, M., Friedberg, A.S. and Moses, R.E. Cloning and characterization of a human cDNA (IMPPLI) sharing Genomics 29 (1), 285-287 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51C protein.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              /CTanslation="MCTRIAFCLMEKISWLCRPRRVCLCPASRPWVSSSACTPSPTRA
/CTanslation="MCTRIAFCLMEKISWLCRPRRVCLCPASRPWVSSSACTPSPTRA
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TAPAAESAPNGLSTVSHDYLKGSYGLDLEAVRGGASHLPHLTRTLATSCRRLHSEVDK
VLSGLEILSKYPEPOGSSPMVTRLLQCONLPOTGEOELESLVLKLSVLKDFLSGIOKKR
LKALODMSSTAPPAPOPSTRKKKTMPVQAFFYKLDVTLGDLTKIGKSQKFTLSVDVEG
GRLVLLRRQRDSQEDWTTFTHDRIRQLIKSQRVQNKLGVVFEKEKDRTQRKDFIFVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                   /codon_start=1
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                                                                                                                                                                                    /cell_type="immortalized fibroblast"
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/db_xref="taxon:9606"
1394 c 1392 g 91.
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Similarity 58.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pesesse, X., Deleu, S., De Smedt, F., Drayer, L. and Erneux, C. Identification of a second SH2-domain-containing protein closely related to the phosphatidylinositol polyphosphate 5-phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inositol polyphosphate 5-phosphatase; SHIP2 gene
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-JUL-1997) X. Pesesse, Interdisciplinary Research Institute, Universite Libre de Bruxelles, Campus Erasme Bidg. (808 Route de Lennik, 1070 Brussels, BELGIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98042455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 239 (3), 697-700 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pesesse,X.
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RKREAFCQLLQLMKNKHSKODEPDMISVFIGTWNMGSVPPPKNVTSWFTSKGLGKTLD
EVTVTIPHDIYVFGTOENSVGDREWLLDLLRGLKFLTDLDYRPIAMOSLMNIKVAVLV
EVERLENGESTENGENTENGAVGVSFMFNOTSFGFVNCHLTSGNEKTARR
KCEHENRISHVSTSSVKTGIANTLGNKGAVGVSFMFNOTSFGFVNCHLTSGNEKTARR
KOHLDLILLSLIGDROLNAFDISLRFTHLFWFGDLNYRLDMDIGELLNYISRKEFEP
LLRVDQLHLEREKHKVFLRFSEEEISFPFYTYKFERGSRDTYAMHKQKPTGVRTNVPSM
LLRVDQLHLEREKHKVFLRFSEEEISFPFYTYKFERGSRDTYAMHKQKPTGVRTNVPSM
CDRILMKSYPETHICNSYGCTDDIVTSDHSPVFGTFEVGVTSQFIISKKGLSKTSDQA
YIEFESIEAIVKTASFTKFFIEFYSTCLEEYKKSFENDAQSSDNINFLKVOWSSROLD
YIEFESIEAIVKTASFTKFFIEFYSTCLEEYKKSFENDAQSSDNINFLKVOWSSSCHE
TLKPILADIEYLDQCHLLLTVKSMDGYESYGECVVALKSMIGSTAQQFLTFLSHRGEE
TLKPILADIEYLDQCHLLLTVKSMDGYESYGECVVALKSMIGSTAQQFLTFLSHRGEE
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FTEASCPLSRLFEEPEKPPPTGRPPAPPRAPREEPLTPRLKPEGAPEPEGYAAPPPK
RTEASCPLSRLFEEPEKPPTGRPAPPRAPPRSATKNKVAITVAPQLGHHRHPRVGE
NSENNPAYYLEGVPHQLLPPEPPSPARAPVPSATKNKVAITVAPQLGHARHPRVGE
GSSDEESGGTLPPPDFPPPLPDSAITLPPSLDPLPGPVVRGRGAEARGPPPKAH
PRPPLPPGPSPASTFLGEVASGDDRSCSVLQMAKTLSEVDYAPAGPAASALLPGPLEL
PRPPLPPGPSPASTFLGEVASGDDRSCSVLQMAKTLSEVDYAPAGPAASALLPGPLEL
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/db_xref="GI:2653424"
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                            /gene="SHIP2"
                                                                                                                                                                                                                                /gene=
                                                                                                                                                                                                                                                                         /tissue_type="hippocampus"
                                                                                                                                                   /note="putative"
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                        /db_xref="SPTREMBL:015357"
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Pred. No. 61;
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SOURCE

COMMENT

/clone="CMB9-4J8" /map="11q" TITLE

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KEYWORDS VERSION

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Best Local Similarity
                                                                                                                                                                FEATURES
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                                                                                                                                  source
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                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Pr
1 (bases 1 to 124635)
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KYAVLVKPPHENIKISHVSTSSVKTGI ANTIGKIKGA (USPENPRGTSEGPVNCHLTSGN
KYAVLVKPPHENIKISHVSTSSVKTGI ANTIGKIKGA (USPENPRGTSEGPVNCHLTSGN
KYAVLVKPPHENIKISHVSTSSVKTGI ANTIGKIGA (USPENPRGTSEGPVNCHLTSGN
EKTARRNQNYLDLILLEREKHK (VFLRSEEELSFPTXY KYEGSRDOTYAMHKQKPTGVR
RKEEEPLLRVDOLILLEREKHK (VFLRSEEELSFPTXY EXPENPRGSENDTYAMHKQKPTGVR
TNPSWCDRILMKSYPETHI I (ONSYGCTDDI VTSDHSPVFGTTEPGVTSOS) FI SKKOLS
TNPSWCDRILMKSYPETHI I (ONSYGCTDDI VTSDHSPVFGTTEPGAVSS) FI SKKOLS
TNPSWCDRILMKSYPETHI I (ONSYGCTDDI VTSDHSPVFGTTENLORD)
KYSDOAY I EFESI BALVKTARRKTKFTLEFFXFTCLEYKKSFENDAQSSDNINFLKVOM
KYSDOAY I EFESI BALVKTARRKTKFTLEFYSTCLEYKKSFENDAGASKARSVSRGSOEPRS
SHRGEETGNIHGSMKVWPTERLGTRELLY ENISIBNDBAGAKSKARSVSRGSOEPRS
GSRKPAFTERASCPLSRLFEEPEKRPPTGRPAPFRAAPREEPLIPPLKPERGAPEPBCV
GSRKFAFTERASCPLSRLFEEPEKRPPTGRPAPFRAAPREEPLIPPLKFREGAPEPBCV
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GSRKFAFTERASCPLSRLFEEPEKRPPTGRPAPFRAAPREEPLIPPRKFREGAFEPBCV
GSRKFAFTERASCPLSRLFEEPEKRPPTGRPAPFRAAPREBPLIPPRKFREGAFEPBCV
GSRKFAFTERASCPLSRLFEEPEKRPPTGRPAPFRAAPREBPLIPPRKFREGAFEPBCV
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GSRKFAFTERASCPLSRLFEEPEKRPPTGRPAPFRAAPREBPLAPRKFREGAFERBERGAPPRAARCP
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PAPETPTAPAAESAPNOLSTVSHDYLKOSYGLDLEAVRGGASHLPSLTRTLATSCRRL
PAPETPTAPAAESAPNOLSTVSHDYLKOSYGLDLEOTGEQELESLVLKLSVLKDELS
HSEVDKYLSGLEILSKVFDQOSSPMYTRLLQQQNLPOTGEQELESLVLKLSVLKDELS
GIQKKALKALQDMSSTAPPAPQPSTRKAKTIPVQAFEVKLDVFLGDLTKIGKSQKFTL
GIQKKALKALQDMSSTAPPAPQPSTRKAKTIPVQAFEVKLDVFLGDLTKIGKSQKFTL
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STVSBARKREAFCQLLCIMKNKHSKODEPDMISVFIGTWNMGSVPPPKNVTSKFTSKG
FIFVSBARKREAFCQLLCIMKNKHSKODEPDMISVFIGTWNMGSVPPPKNVTSKAMGSLWII
LGKTLDEVTVTIPHDIYVFGTOENSVGDREWLDLLRGGLKELTDLDYRPIAMGSLWII
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PGPLELQPPRGLPSDYGRPLSFPPPRIRESIQEDLAEEAPCLQGGRASGLGEAGMSAW
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1 1466 c 1448 g 890 t
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                                                                                                                                                                                                                                 2001 this sequence version replaced gi:12246850
                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                    Location/Qualifiers
/chromosome="11"
                                        /db_xref="taxon:9606"
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pred. No. 60;
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ORIGIN

BASE COUNT 31089 a 29103 c 30489 g 33954 t

Query Match
29.3%; Score 36.6; DB 9; Length 124635;
Best Local Similarity 58.9%; Pred. No. 34;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps

0;

Search completed: September 7, 2002, 18:26:54

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OM nucleic - nucleic search, using sw model
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Eukaryota: Metazoa: Primates; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

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Moyel receptor dna useful for cancer chemotherapy

substances potentially useful for cancer chemotherapy

substances potentially useful for cancer chemotherapy

patent: DE 1984779-C 4 03-FEB-2000;

substances potentially useful for cancer chemotherapy

patent: DE 1984780RSCH (DE)

patent: DE 198479-C 4 03-FEB-2000;

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/organism="Homo sapiens" Location/Qualifiers

FEATURES	JOURNAL	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	RESULT 2 AX026091 LOCUS DEFINITION ACCESSION VERSION	Qy 2821 ag    Db 2821 AG	2101 gcacgg   2101 gcacgg   2101 gcacgg   2101 gcacgg   2161 ggacca   2161 ggacca   2161 ggacca   2261 aagcc   2281 aagcc   2281 aagcc   2341 ggggtc   2341 ggggtc   2341 ggggtc   2341 TrTC   2521 tttt   1   1   1     2521 tttt   2521 ttt	J. J. J. J.
1 2380	Patent: DE 19847779-C 3 03-FEB-2000, Patent: DE 19847779-C 3 05-FEB-2000, Patent: DE 1984777-C 3 05-FEB-2000, Patent: DE 198477-C 3 05-FEB-2000, Patent: DE 19847-C 3 05-FEB-2000, Patent: DE 1984	1 (bases 1 to 2380) Nucler-Schilling,M., Krammer,P. and Orén,M. Nucler-Schilling,M., Krammer,P. and Orén,M. Novel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for cancer chemotherapy Schinghappers potentially useful for cancer chemotherapy	human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX026091 2380 bp DNA linear PAT 16-SEP-2000 Sequence 3 from Patent DE19847779. AX026091 GI:10187522	gacgtg 2827          GACGTG 2827	geacygaacacaccctgaggccagccctgagccgagcagccccaggaggagctgcctcttctcccac 2160 [11111111111111111111111111111111111	
-	901 TTTTTTTAAAGAAAATTGGCCAGGAAATAATGAGTAAUGAAUGAAAGAAAATTGGCCAGGAAATAATGAGTAAUGAAGAAAAATTGGCCAGGAAATAATGAGTAAUGAAGAAGAAAGAAAGAAATAATGAGTAAUGAAGAAGAAAGA	ATAGTGACTTTGAZ  aaaattggccagg	781 F	Db 661 ANTTGGGAAGGGAAGGGAAGAGAGAGAGAGAGAGAGAGAG	601 TC	C 568  C 568  C 568  C 568  C 68; Pri  C 77777777777777777777777777777777777	wref="taxon:9606"

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with rhis sequence was finished above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= one plasmid subclone or more than one Mil sequencing problems, such assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em:, EMBL; Sw:, database can be found at http://www.sannar.ac.u//nrointer/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silentar/silenta
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This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The Location/Qualifiers
                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 of Pieter de Jong. For further details see
                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Human DNA sequence from clone RPI1-399019 on chromosome 10,
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Malia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 187313)
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Qy 541 cacat	y 301 gaac; b 142269 GAAC; b 142269 GAAC; l       b 142329 AAGA  Db 142329 ACT#  Db 142389 ACT#  Db 142449 TAAW	Oy 1 tgaggac	source  misc_feature  Misc_fea
pacatagtgagttgctggctacaaccccciiiiiiiiiiii	paggataattagacgtagggtagagggtaggggtaggggaaggygyijiiiiiiiiiiiiiiiiiiiiiiiiii	ctctcaggaatatgctggraaadcadadcallillillillillillillillillillillillilli	J187313  /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="10" /clone="110" /clone=lib="RPCI-39019" /clone=lib="RPCI-39019" /clone=lib="RPCI-311.2" /clone=lib="Reciperate" /clone=lib="R

78 14274 84 14286 96 14288 97 1429 1429 1429 1429 16 17 10 10 10 10 10 10 10 10 10 10 10 10 10
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868 868 9928 9928 9988 3048 40 40 13168 3108 43228 43228 43228 43228 143341 143441 143
58 58 88 88 88 88 88

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Db 144789 GGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTCGAAAAAGTTATATGGGG 144848
                                                                                                                             Db 144729 AGATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGT 144788
                                                                                                                                                                               Db 144609 AGAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCAAAGCCAAAGGTCCGCTCCGGCG 144668
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2548 geettgteteeetteegggaattetetetttaagaetgtaagtegetgeetgagtggttt 2607
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Db 143829 TCACCCTGACTTCTCCCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC 143888
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              301 gaacttgaggataattagacgtacgtgggtagagggtagggggaagggggtatggcataga 360
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301 GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGGTATGGCATAGA 360
                                                    241 CTAAGATTATTTGACCÁTGAÁACATATGTCTCCCCACAAAGCÁCÁTÁTTCCTATCTCCTT 300
                                                                 241 ctaagattatttgaccatgaaacatatgtctccccacaaagcacatattcctatctcctt 300
                                                                                                       181 TAAGGGCCCTGAGAAGTTTTGGATTAAGAAAGTTTTCAAATTAAAGTAACCCAGAATTTT 240
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Local Similarity 87.0%; Pred. No. 0;
Docal Similarity 87.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller-Schilling,M., Krammer,P. and Oren,M. Rovel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 1 03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3212)
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/db_xref="taxon:9606"
784 c 809 q 84
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y 1321 tcaccagagcccyccy 1111111111111111111111111111111	1200 CTGCALCARA	1141 gcagagettggtggacgatgccaaaggaartactgacacccciffififififilililililililililililili	1020 GAAGAAATGTCAACTGAGAGGAAGCCTGAAGAGAGAGAGGAGAGGAAAGGATAA 1020 GAAGAAAATGTCAACTGAGAGGAAGGAAGCCTGAAGAGAGAG	31 gtgatggaaagcctcaggayyy Common Hillillillillillillillillillillillillill	901 acaagcctatcaacacctacaagactggtggtaagrucaggtliiliiliiliiliiliiliiliiliiliiliiliilii	GCACTAACAGTCTACAGATGCAACAGCTCGAACAGCTCAACAGTCTACTGAAAGGTCGAACACTCAACAGGTGCAACACAC	TITITION OF THE PROPERTY OF TH	98-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1		rTTCCCCTTTTTTTCTCTCTTCTTCTTT	01 cettteccetttttttttttlllllllllllllllllll	41 cacatatgtgagttgctggcttataaccccctiliiiiiiiiiiiiiiiiiiiiiiiii	81 taagtttaataatcactcatccccccyyyccarriii	21 actaaccatct-ty-comments	61 aagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctattctlillillillillillillillillillillillillil	† ; † † † † † † † † † † † † † † † † † †

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3180 CAGAAATGCCAGCTTGCAGATGGCTAATCAAAG 3212
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                                                                     Submitted (26-MAY-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
                                                                      Development, Corporation Ltd., PO Box
Overlaps with X81335, 6 X82279-X82286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of a silencer, enhancer, and basal promoter region the human CD95 (Fas/APO-1) gene DNA Cell Biol. 14 (11), 931-937 (1995)
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
                                                                                                                                                                                                                                                                                                   H.Sapiens CD95 gene 5' flanking region
                                                                                                                                                                                                                                                                interferon; CD95 gene; silencer.
                                                                  Location/Qualifiers
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/note="basal promoter"
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/map="q24.1"
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/db_xref="taxon:9606"
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tive 0; Mismatches
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FEATURES COMMENT

source

REFERENCE

JOURNAL MEDLINE

TITLE

AUTHORS TITLE

JOURNAL

Direct Submission Rudert, F.H.

(bases 1 to 2344)

REFERENCE

AUTHORS

KEYWORDS SOURCE

X87625.1 GI:902311

ORGANISM

Homo sapiens

VERSION

DEFINITION ACCESSION HSCD955FR

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                                               protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Fas antigen.
                                                                                                                                                                                                                                       Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Tel:076-234-4424, Fax:076-234-4480)
                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2165)
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                                                                                                                                                                                                                                                                                                                                                                              Wada, N.,
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                                                                                                                                                                                                                                                                                                                               factor for interleukin-6 expression upon influenza virus infection J. Biol. Chem. 270 (30), 18007-18012 (1995)
                                                                                                                                                                                                                                                                                                                         95355401
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                                                     1167 gaatactgaaacctttagtgtgtccagtctggaactgcatccaaattcaggttcagtaat 1226
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781 GATGTCATTATCCAAACATACCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCT 840
                                                                                                                                             1047 ctgaaggatgaacagtgggctaagcaaagggttattaatgtgtttattaatgggttgaatc 1106
                                                                                                                                601 CTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTATTAATGTGTTATTAATGGGTTGAATC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1715; Conserv
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                     481 GGTGGTAAGTGCAGTGACAGATGCAAAACACAGGGTGATGGAAAGCCCTCAGGAGGGTAA 540
                                                                                                                                                                                                                               927 ggtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaa 986
                                                                                                                                                                                                                                                                                                          361 TTGTGTCTATTAGATGCTCAGAGTGTGTGCACAAGGCTGGCACACCCAGGGTCTTCCTCA 420
                                                                                                                                                                                                                                                                                                                                                               747 aaaatttgcagagataatacagagaatgcccatataccatcctccttatcccacttcttt 806
                                                                                                                                                                                                                                                                                                                                                                                            GAATACTGAAACCTTTAGTGTGTCCAGTCTGGAACTGCATCCAAATTCAGGTTCAGGTAAT 780
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                                                                                                                                                                                                                                                                TGCACTAACAGTCTACTGAAAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACT 480
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                      APO-1 gene; apt gene.
                                                                    human.
                                                                                                       H.sapiens APT gene, exon
X81335
                                                                                      X81335.1 GI:537410
                                                                                                                                HSAPT1
                                                                                                                    1877 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (03-SEP-1994) P.H. Krammer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center, Tumorimmunology Programm, Im Neuenheimer Feld 280,
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x81338 1:145. .253,x81339 1:552. !613,x81339 1:766. .828,

x81340 1:79. .161,x81341 1:255. .279,x81342 1:103. .1757)
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151. .261
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x81338.1:145. .253, x81339.1:552. |.828, x81340.1:79. .161,

x81341.1:255. .279, x81342.1:103. |.1757)
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x81340.1:79. . 161, x81341.1:255. . 279, x81342.1:103. . 1757)

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          1107 taattgggaagggagaggttgcagagtgaggtgcagagcttggtggacgatgccaaag 1166
 660
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                                                                                           cotaacctagatttgagggcccaaacaggctccagaagaaaatgtcaactgagaggaagc 1046
                                                                                                                                                                   TGGCACTAACAGTCTAACAGGTGGAACAGAGACAAGCCTATCAACACCTAC-AGACT
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                                                                                                                                    9gtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaa
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                                        CCTAACCTAGATTTGAGGGCCCAAACAGGCTCCAGAAGAAAATGTCAACTGAGAGGAAGC
TAATTGGGGAAGGGAGAGGTTGCAGAGTGAGGTGCAGAGCTTGGTGGACGATGCCAAAG
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X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,
X81340.1:79. .161,X81341.1:235. .279,X81342.1:103. .>1757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /usedin=x81335:HsmRNA6
join(1708. 1810,X81336.1:155. .320,X81337.1:146. .283,
X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,
X81340.1:79. .161,X81341.1:255. .279,X81342.1:103. .>1757)
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/gene="APT"
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DEFINITION H.sapiens Fas, Apo-1 gene (promoter and exon I).
                                                                                         1680 CTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCGG 1715
                                                                                                       2127 ctggctgcccaggcggagctgcctcttctcccgcgg 2162
                                                                                                                                          1620 AGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGGCACGGAACACACCCCTGAGGCCAGCC
                                                                                                                                                      2067 agtgacttggctggagcctcaggggcgggcactggcacgggaacacaccctgaggccagcc 2126
                                                                                                                                                                                                 1560 CGCAAGAGTGACACAGAGTGTTCAAAGACGCTTCTGGGGGAGTGAGGGAAGCGGTTTACG
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1247 ccttctgtaaaattcatgctaaactacctaagagctatctaccgttccaaagcaatagtg 1306
                                                                   1187 tgtccagtctggaactgcaatccaaattcaggttcagtaatgatgtcattatccaaacata 1246
                                                                                                                                     1127 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 1186
                                                                                                                                                                                                      427 TGTCCAGTCTGGAACTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATA 486
                                                                                                                                                                                                                                                    187 ATGCAAAACACAGGGTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGC
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                                                                                                                   TTGCAGAGTGAGGTGCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham, Univ. of Alabama, 701 South 19th Street, UAB Station, LHRB 473, Birmingham, AL 35294-0007, USA Related sequences: M57454 and X63717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Cheng, J., Liu, C., Koopman, W.J. and Mountz, J.D.
Characterization of human Fas gene. Exon/intron organization and
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1075. 1496
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a 421 c 423 g
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                                                     VERSION
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Diagnosis of diseases associated with the immune system
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2393 ctcagacgtaggaaataagtcagcaccgaagcagtagttaagccagaaggacTcGgaagaa 345
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2753 aaacttgagcetgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 705
2753 aaacttgagcagcctgttttgaaaagtcccrccrcAaAArrGCCAGCTTGCAGArGGCT 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contact: Michael Olivier, pavid R. Cox contact: Michael Olivier, pavid R. Cox stanford Human Genome Center Medicine A stanford University and F1., palo Alto, Stanford University and F1., palo Alto, 105 Miranda Aves 2nd F1., palo Alto, 105 Miranda Aves 20.5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (650) 320-5800
Tel: (650) 320-5801 stanford edu
Tel: (650) 320-5801
Tel: (650) 320-
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Jinear STS 30-MAR-2

JOSEPH DNA Linear tagged site.

JOSEPH Human Homo Sapiens STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                   Buffer:
                                                                                                                                                                                                                            prepared with primer pairs provided by Sandoz, derived from H86126
prepared with primer pairs provided by Sandoz, derived from H86126
prepared with primer pairs provided by Sandoz, derived from H86126
prepared with primer pairs provided by Sandoz, derived from H86126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerization:
pCR Cycles:
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rotal vol:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                each 200 uM
0.05 units/ul
10 ul
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62 degrees C for 30 seconds
72 degrees C for 30 seconds
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50 mM
20 mM
8.3
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REMARK
COMMENT
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AUTHORS
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                 RESULT 13
BC012479
                                                                                                                                                                                                                                     ORGANISM Homo sapiens
                                                                                                                                                                                                                                                                                                   DEFINITION
Clone distribution: MGC clone distribution information can be found the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                         В
                                                                              Email: Color New Wesk
Tissue Procupement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                             Strausberg, R.
Direct Submission
Stausberg, R.
Submitseton
Gene Collection (MGC-2001) National Institutes of Health, Mammalian
First Tute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                        2793 atgccagcttgca-gatggctaatcaaagag 2822
                                                                                                                                                                                                                                                                                                                  241 ATGCCAGCTTGCAGGATGGCTAATCAAAGAG 271
                                                                                                                                                                                                                                                                                                                              2733 99c9cctattattg9ccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaa 2792
                                                                                                                                                                                                                                                                                                                     181 GCGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 270; Conserva
                                                                                                                                                                                                                                                                                                                                                          Primer_bind
BASE COUNT bind
ORIGIN
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HOMO SEPIENS, SIMILAR to 2719 bp
Superfamily, Member 6, clumor necrosis factor receptor
HCM13470 cds. Member 6, clone MGC:21432 IMAGE:4514272, MRNA,

MGC:21432 IMAGE:4514272, MRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                  2553 gtctcccttccgggaattctctctttaagactgtaagtcgctgagtggctgagtgttcattt 2612
                                                                                                                                                                       Taryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, (bases I to 2719) Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    BC012479
                                                                                                                                                                                                                                                                                                                                                                                                          1 GTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGGCCTGAGTGGTTTCATTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         llarity 9.2%; Score 259; DB 11; I
Conservative 0; Mismatches 0;
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93 c 105 g 125 t
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/Map=#10" taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
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REFERENCE
AUTHORS
                                         JOURNAL
                                                       TITLE
                                                                                                      SOURCE
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VERSION
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                                                                                                                                           RESULT 14
HSA279011
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                                                                                                                                                                                                      Дb
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutheleostomi, Nambela, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Somatic mutacions of the CD95 gene in human B cells as a fine-effect of the germinal center reaction
                                                                                                                                                                           2158 <sup>cgcgg</sup> 2162
                                                                                                                                                        2098 ctggcacggaacaccactgaggccaggccctggctgcccaggcggagctgccttctccc 2157
                                                                                                                                                  181 CTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCC 240
                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                           121 CTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTTGGAGCCTCAGGGGCGGCA 180
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 8.7%; Score 245; DB 9; Local Similarity 100.0%; Pred. No. 4.6e-51;

Matches 245; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          1978 ggcttttcgtgagctcgtctctgatctcgcgcaagagtgacacaggtgtcaaagagcg 2037
                                                                                Homo sapiens
                                                                                                                                                                                                                           61 GCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACG 120
                                                                               HSA279011
HOmo sapiens partial CD95 <sup>702</sup> bp DNA
Tinear PRI 02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                           . Fas; CD95 antigen; CD95 gene.
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Passed the following selected for full length sequencing selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                   /clone="MGC.21432"...
/tissue_type="9432 IMMGE:4514272"
/lab_host="MIH_MGC_93" transitional cell papilloma"
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REFERENCE
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                                                                                              RESULT 15
HSA279012
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                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-SEP-2000) Muschen M., Department of Immunology, 50931 Submitted (19-SEP-2000) Kri E4 R705, Joseph-Stelzmann-Str. 9, 50931 Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
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KEYWORDS
                                                                                                                                                                                                                                                                                                                      2007 cgcaagagtgacacacaggtgttcaaagacgcttctgggggagtgaggggaagcggtttacg 2066
                                                                                                                                                                                                                                  Local Similarity 100.0%; Pred. No. 8!8 (Local Similarity 100 o; Mismatches 1es 216; Conservative
                                                                                                                                                                61 CGCAAGAGTGACACAGGTGTTCAAAGACGCTTCTGGGGAAGTGAGGGAAGCGGTTTACG 120
  702 bp DNA linear pRI 02-APR-2001
HSA279012 partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
Homo sapiens partial CD95 yene for CD95 antigen (Apo-1 Fas), exon
1279012 GI:13539240
AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13539240 AJZ79012.1 GI:13500 AJZ79012.1
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/note="Hodgkin's disease tissue"
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282. >313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="CD95 antigen"
/protein_id="CAC35539.1"
/protein_id="GI:13539239"
/db_xref="GI:13539239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLGIWTLLPLV"
314. >702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"CD95"
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100.0%; Pred. NO. 8!8e-44;
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/db_xref="taxon:9606"
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/gene="CD95"
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/gene="CD95"
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Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mischen, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, K. and Muschen, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission 2000) Muschen M., Department of Immunology, 50931 Submitted (19 SEP 2000) FI E4 R705, Joseph-Stelzmann-Str. 9, 50931 Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str.
                                                                                                                                                                                                                                                                                                                                                                    1947 gaggetteetteecateeteetgaceaceggggettttegtgagetegtetgateteg 2006
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                                                                                                                                                                                                                          7.6%; Score 216; DB 9; Length 70; Match 100.0%; Pred. No. 8.8e-44; Indels Local Similarity 100.0%; Mismatches hes 216; Conservative
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1 GAGGETTCCTTCCCATCCTGACCACCGGGCTTTTCGTGAGCTCGTCTCGATCTCG 60
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Search completed: September 7, 2002, 18:35:34

Sequence:

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                       Score
                               129
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1 tgaggactctcaggaatatg......tggctaatcaaagagacgtg 2827
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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US-08-444-231-18
US-08-152-443A-18
US-08-152-443A-18
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sequence 18, Appli
sequence 1, Appli
sequence 1, Appli
sequence 1, Appli
sequence 16, Appl
sequence 14, Appl
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sequence 10, Appli
sequence 10, Appli
sequence 3, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 19, Appl
Sequence 25, Appl
Sequence 18, Appli
Sequence 18, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 9, Appli
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Best Local S
                               RESULT 2
US-08-444-231-18
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Result

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18 19 20 21 22 23 23 24 25 26

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US-09-018-584A-19
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Sequence 27, Appl
Sequence 27, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 10, Appl
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Sequence 3, Appli
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Sequence 10, Appl
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ORGANISM: Homo sapiens
FEATURE:
EARTURE:
NAME/KEY: CDS
LOCATION: (221)..(1228)
LOCATION: INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
VOLUME: 267
ISSUE: 15
PAGES: 10709-10715
PAGES: 1992-05-25
DATE: 1992-05-25
DATABASE EXTRY DATE: 1996-07-19
DATABASE EXTRY DATE: 1996-07-19
DATABASE EXTRY DATE: 1996-07-19
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: ANTISCHOOL OF ANTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
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                                                                                                                                                                                gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                     gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 2127
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Sequence 18, Application US/08152443A Patent No. 5663070
                                           RESULT 3
US-08-152-443A-18
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; LOCATION:
US-08-444-231-18
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
TRANDEDNESS: sinc).
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                                                                                                                                                                                              2034 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 2093
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FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDI, SUSAN K.
REGISTRATION NUMBER: 33,943
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
TELEPAX: 776141
                                                                                              121 CTCCCGCGG 129
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                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE: 18-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 755 Page M
CITY: Palo Alto
STATE: Callfornia
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                4.6%; Score 129; DB 1; L
100.0%; Pred. No. 2.3e-26;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                       Length 2471;
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Sequence 1, Application US/08219237B
Patent NO. 5874546
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: 170H, Naoto
APPLICANT: 170H, Naoto
APPLICANT: 170H, Naoto
APPLICANT: 170H, Naoto
APPLICANT: 170HARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
                                                                                                                                                    US-08-219-237B-1
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Best Local Similarity 100.0%; Score 129; DB 1; L
Matches 129; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                      2094 99cactggcacggaacacacctgaggccagccctggctgcccaggcggagctgcctctt 2153
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: SHAPIRO, JOHN P.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
ADDRESSE: MORISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                      61 GCACTEGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                1 GACGOTTOTOGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGGTGGAGCCTCAGGGGCG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMpe
OPERATING SYSTEM: PC-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: 435
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,9
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O:
FILING DATE: 15-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304-1018
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195..1136
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243
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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## us-09-834-291-4.rni

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in in the street	FEATURE: NAME/KEY: polyA_site NAME/KEY: 25182523 IOCATION: 25182523 Dentification method: to an established consensus TOBNITETICATION METHOD: to an established	rsj Fil	(EY: IFICA' IFICA'	PEATURE: mat_peptide NAME/KEY: mat_peptide LOCATION: 243119 by similarity with known sequence or IDENTIFICATION METHOD: by similarity with known sequence or IDENTIFICATION METHOD: to an established consensus	REATURE: sig_peptide NAME/KEY: sig_peptide NAME/KEY: 195242 LOCATION METHOD: by similarity with known sequence or LDENTIFICATION METHOD: by similarity with known sequence or by s	FEATURE: CDS NAME/KEY: CDS LOCATION: 1951202 LOCATION METHOD: by similarity with known sequence or IDENTIFICATION METHOD: to an established consensus IDENTIFICATION METHOD:	ADDRESSEE: James W. Hellwege STREET: p.O. Box 2266 Eads Station CITY: Arlington STATE: Virginia COUNTY: Virginia COUNTY: USA ZIP: 2202 ZIP: 2202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: PATON DATA: CORRENT APPLICATION UNTA: P94 FILING DATE: 28-MAR-1994 FILING DATE: 28-MAR-1994 FILING DATE: 28-MAR-1994 FILING DATE: 28-MAR-1992 FILING DATE: 105 ONTO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS	

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US-08-468-560C-1
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COMPUTER READABLE FORM:
COMPUTER STATEM POR COMPATIBLE
COMPUTER: ILDAPY disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.30
SOFTWARE: PALENTION NAME: US/08/468,560C
APPLICATION NUMBER: US/08/468,560C
APPLICATION: 435
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
FILING DATE: 08-JUN-1995
FILING DATE: 08-
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TITLE OF INVENTION: ANTIGEN
OF SEQUENCES: 11
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
CITY: FALLS CHURCH
CITY: FALLS CHURCH
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APPLICANT: TTOH, NAOCO
APPLICANT: YONEHARA, Shin
APPLICANT: YONEHARA, Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-205-8050
TELEPAX: 703-205-8050
TELEPAX: 708-205-8050
TELEPAX: 708-205-8050
TELEPAX: 708-205-8050
TELEPHONE: 708-2050
TELEPHONE: 708
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ORGANISM: Homo
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NAME/KEY:
LOCATION:
                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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                                               FEATURE:
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LOCATION:
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195..242
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E: CDNA to mRNA
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243..1199
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195..1202
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1831..1836
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2352..2357
               polyA_site
2518..2532
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US-08-468-560C-1

Query Match

Best Local Similarity 100.0%; Score 129; DB 4; 1

Matches 129; Conservative 0; Mismatches 0;

DB 4; Length 2534;

2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093

1 GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG 60

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APPLICANT: NAKAMURA, No. 630639510

APPLICANT: NAKAMURA, No. 630639510

ITILE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
CURRENT APPLICATION: NOVEL Fas ANTIGEN DERIVATIVE
CURRENT APPLICATION NUMBER: US/09/180,100
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1999-11-02
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2534
TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                         Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 129; Conservative
                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
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                                                                                                                                                                                                                                                                                                                                                            2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
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Patent No. 6306395
                                                                                                                                                                                                                                                                                 61 ggcactggcacggaacaccaccctgaggccagccctggctgcccaggcggagctgcctctt 120
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1466 GCATAGATA 1474
                  1406 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTATCTCTTTTAACTACTT 1465
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen 29,768
REGISTRATION NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 3047.
TELEPHONE: (703)836-9300
TELEX: 89149
INFORMATION FOR SEQ ID NO: 14:
LENGTH: 7218 base pairs
TVDE: (71218 base pairs
                                                              Matches
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                         694 acattitititattiaaatgaacttiticattitggaatagtititaggatticaaaaaatti 753
                                                                                  634 attentectionettacctotectttectteceteacaccccttttccttccttctttt 693
                                                                                                                                                   514 aatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataattcacac 573
                                                                                                                                                                                                                  454 thtggctacatttttttatttgtaaagtaagtttaataatcactcatctcactgggctat 513
                                                                                                                                                                                                                                                        394 tttaattootgactotgotatttattaactaaccatctttgccaatgttgcttaagcttt 453
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
PILING DATE:
APPLICATION NUMBER: EP
FILING DATE: 26-AUG-19
                                                                                                                                                                                                                                                                                        Match 2.8%; Score 79.4; DB 1; Length 7218; Local Similarity 5.4%; Pred. No. 4.9e-12; Length 7218; Les 20; Conservative 224; Mismatches 125; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARDE. Date: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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US-08-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367

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CLONE: pTZgpt-F1s
US-08-232-463-14
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CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 14:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                             867 tggcactaacagtctactgaaaggtggaacagagacaagcctatcaacacctacaagact 926
                        1107 taattgggaagggagaggttgcagagtgcagagcttggtggacgatgccaaag 1166
                                                      1047 ctgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatc 1106
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987 cotaacctagatttgagggcccaaacaggctccagaagaaaatgtcaactgagaggaagc 1046
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                                                                                                                                                                                                                                                                                                                                      y Match 2.4%; Score 67.4; DB 1
Local Similarity 8.0%; Pred. No. 1.2e-08;
nes 35; Conservative 228; Mismatches 17
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                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                     174;
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US-08-836-022A-10
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                                                                                                                                                                                                                                                                                US-08-836-022A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                             Db 16048 CCGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACGCGGACATGTACAGA 16107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1022 GTGAGCGTATGGCAAAC 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1167 gaatactgaaacctttagtgtgtccagtctggaactgcalccaaattcaggttcagtaat 1226
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                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                            Best Local Similarity Matches 93; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weitzman, Matthew TITLE OF INVENTION: Improved Adenovirus Virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: PATENTIN PATA:
OPERATION DATA:
APPLICATION NUMBER: US/08/836,022A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
16168 TTTACAACGTCGTGACTGGGAA 16189
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Spring House CITY: Spring House Pennsylvania
                                                                16108 GCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGT 16167
                                                                                2174 gctcgagaagtactagtggccacgtgggccgtgcaccttaaggctttagggtcgctggagg 2233
                                                                                                                                                 2114 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacaga 2173
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                            2234 gggaccccggttggagagaga 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1947
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                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bak, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spring House Corporate Cntr, P O Box 457
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Fisher, Krishna J.
Chen, Shu-Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                      19307 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                                     2.2%; Score 63.6; DB 3; Length 19307; 65.5%; Pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNVPN.008PCT
                                                                                                                                                                                                            0;
                                                                                                                                                                                                          Mismatches 49;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                       0; Gaps
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RESULT 11
US-08-836-022A-3/c
; Sequence 3, Application US/08836022A
; Patent No. 6001557
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:

NAME: BAK, MATY E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: GNVPN

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19307 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                    16168 TTTACAACGTCGTGACTGGGAA 16189
                                                                                                                                                           16108 GCTCGAGAAGTACTAGTGGCCACGTGGGCCCTGCACCTTAAGCTTGGCACCTGGCCGTCGT 16167
                                                                                                                                                                                                                                  16048 CCGCCCGCCTGCAGCTGGCCCCATCGATACCCGTACCTCGCGACCCGCGGACATGTACAGA 16107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-427-048A-10
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                                                                                                                                      2234 gggaccccggttggagagagga 2255
                                                                                                                                                                                 2174 gctogagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggagg 2233
                                                                                                                                                                                                                                                        2114 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09427048A Patent No. 6203975 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             Match 2.2%; Score 63.6; DB 4; Length 19307; Local Similarity 65.5%; Pred. No. 2.7e-07; es 93; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER RADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC COMPATIBLE
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Improved Adenovirus Virus and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/836,022 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Spring House Corporate Cntr, P O Box 457 STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weitzman, Matthew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, James M.
Fisher, Krishna J.
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US-09-427-048A-3/c
; Sequence 3, Application US/09427048A
; Patent No. 6203975
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                   2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                                                                                                                                                                                                  2235 ggaccccggttggagagagga 2255
                                                                                                                                                                                                                                                                                                        2920 CTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                                                                                                                                                                                                                                         2175 ctcgagaagtactagtgggccacgtgggccgtgcaccttaagctttagggtcgctggaggg 2234
                                                                                                                                                                                                                                                                                                                                                                           2980 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 2921
                                                                                                                                                                                                                                                                                                                                                                                            2115 ctgaggccagccotggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215.540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
Weitzman, Matthew
Invention: Improved Adenovirus Virus and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Trustees of the University of Pennsylvania APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
                                                                                                APPLICANT: Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9972 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                          Wilson, James M.
Fisher, Krishna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                             Chen, Shu-Jen
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2%; Score 62.6; DB 3; Length 9972; 65.2%; Pred. No. 3.4e-07; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/836,022A
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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APPLICATION UNMER: 08/836,022

APPLICATION UNMER: 08/836,022

FILING DATE: CUDKNOWN>

ATTORNEY_AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION UNMER: 31,215

REGISTRATION UNMER: 31,215

REFERENCE/DOCKET NUMBER: GNVPN.008PCT

REFERENCE/TOOK INFORMATION:

TELEPONE: 215-540-5818

TELEPONE: 215-540-5818

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
SEQUENCE STANDEDNESS: double
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 2, Application US/08801344 patent No. 6087140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2175 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggaggg 2234
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CORRESPONDENCE ADDRESS: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2235 ggaccccqgttgqagagagga 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                                                                                                                                                                          TITLE OF INVENTION: MICROSTAL PRODUCTION OF 1,2-PROPANEDIOL TITLE OF INVENTION: FROM SUGAR
                                                                                                                                                                                                                                                                                                                       APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
APPLICANT: Altaras, Nedim E.
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                               STREET:
                                                                                                                                                                 ADDRESSEE:
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914
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CITY: Spring House
STATE: Pennsylvania
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Similarity 65.2%;
92; Conservative
                                                                                        Madison
                                                                                                                               8000 Excelsior Drive, Suite 401
                                                                                                                                                                 pewitt Ross & Stevens S.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 49; Indels
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pred. No. 3.4e-07;
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ORIGINAL SOURCE:
ORGANISM: Vec.
US-08-801-344-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-498-599-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPE PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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NAME: Sara, Charles S.
PELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEPHONE: 608-831-2100
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/801,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCCGCGGACATGTACAGAG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens S.C.
ATREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MI
                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATEM: PC-DOS/MS-DOS

OPERARE: PatentID Release #1.0, Version #1.30

SOFTWARE: PatentID DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 53717-1914
                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                              CITY: Madison
                                                                            APPLICATION NUMBER: US/09/498,599 FILING DATE:
                                                            CLASSIFICATION:
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Altaras, Nedim E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%; Score 62.4; DB 3; Length 4476; 75.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                    MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL FROM SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09820.037
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                                09820.037
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US-08-306-691B-19
                             INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-306-691B-19
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Vect
US-09-498-599-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08306691B
                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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Best Local Similarity
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ELECTAY: 608-831-2106
SEQUENCE CHARACTERISTICS:
ELENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: 55
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/306,691B FILING DATE: September 15, 1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Calabretta, Bruno
APPLICANT: SKOTSKI, TOMASZ
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                           double
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Search completed: September 7, 2002, 18:29:19 Job time: 29253 sec

Plasmid pF58 contg

Human

metastasis a

Human immune syste

immune syste immune syste

Human reproductive Human immune syste Human immune/haema Murine mOCIL genom Human immune syste Retinoblastoma bin

genom

Human polynucleoti Human nervous syst Human immune/haema Human DNA marker c Human immune/haema Tumour suppressor

## us-09-834-291-4.rng

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                    1372.8
879.4
856.8
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161
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2827
1 tgaggactctcaggaatatg......tggctaatcaaagagacgtg 2827
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Copyright (c) 1993 - 2000 Compugen Ltd.
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NSIDS1/gcgdata/h
SIDS1/gcgdata/h
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| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1983.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1985.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1995.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1991.DAT:*
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| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1995.DAT:*
| SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA2001.DAT:*
| SIDSI/g
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     48.6
31.1
30.3
6.7
5.7
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4.6
4.6
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                                    1608
1608
1608
859
266
2551
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ABL34419
ABL34418
AAC98177
                                        AAZ88700
AAC61798
AAQ93879
             AAQ29959
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Human immune syste
Human colon cancer
Human colos recepto
Human coding a hum
DNA encoding a hum
Eas-delta-TM cDNA.
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556
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24259
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/note= "Fas gene promoter region"
147..151
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                      /function= GF1 transcription factor binding site /note= "Claim 7"
                                                                      /function= Myb transcription factor binding site
/note= "claim 9"
349..353
                                                                                                                              /function= EBP20 transcription factor binding site 272...276
                                                                                                                                                                             168..174
                                                             /*tag=
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AAT16303
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Human c-fms oncoge
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Murine LOBO homolo
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EP-892047 Seq ID 4
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Human nervous syst
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Human polynucleoti
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Query Match
Best Local Similarity
                                                                                                Matches 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          827 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 886
                                    767 agagaatgcccatataccatcctcattatcccacttctttttgtgtctattagatgctca 826
                                                                                                                                                        A novel DNA segment (AAT34162) has an isolated sequence region defined as the Fas gene promoter region. This includes a number is also included. The DNA segment was isolated from a human pertide corresponding to nt 23-346. It can be combined with a structural transcription factor binding sites. A coding sequence for placental DNA library using a 32P-labeled segment from a human gentide corresponding to nt 23-346. It can be combined with a structural transcription factor binding sites. The promoter region can be too find the gene is under the transcriptional control of the a means of treating Fas mediated apoptosis disorders such as malionancies and antrimmune diseases
                                                                                                                               Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;
                       7 acagagatgccctataccatccttcttatcccacttctttttgtgtctattagatgctca 66
                                                                                                                                                                                                                                                                                                          Claim 11; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                             Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas-mediated
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-354527/35
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                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR99471
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                                                                                                 48.68;
99.48;
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1497..1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1479..1469
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/note- "claim 5"
1037..1043
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521..525
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                                                                                    0;
                                                                                            Score 1372.8; DB 17; Length 1608;
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                                                                                            1787 gtgagcatgccagccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaa 1846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 2392.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                     Olek A,
                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and including eyeration, arteriosclerosis, anaemia, cancer, acute myeloid eyeration, arteriosclerosis, anaemia, neurofibromatosis, macular degeneration, arteriosclerosis, anaemia, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel alseases. The present sequence is a gene of the invention.
                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                   cytosine methylation
                                                                                                                                                        Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
   Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 other;
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                   642 AAACTACAACAAAAACCTTTAAAAAAAACAAAAAACCGACTCTCGAAAATCCTCACCTAAA 583
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                  Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German.
                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                      WPI; 2002-130909/17.
                                                                                                                                                        Olek A, Piepenbrock C,
                                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           779 tataccatcctccttatcccacttcttttgtgtctattagatgctcagagtgtgtgcac 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloj rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 aaggttggtacgtttagggtttttttttatggtattaatagtttattgaaaggtggaatag 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.3%; Score 856.8; DB 24; 76.7%; Pred. No. 4.6e-226; ative 0; Mismatches 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 1608;
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                                                                       DR XXX PRX XXX PX XX PX XX PX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1799 gccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaaccctgactcctt 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038 gttattgtaggaacgtttcgggataggaatgtttatttgtgtgtaacgaattttgatttttt 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1859 cctcaccctgacttctccccctccctacccgcgcgcaggccaagttgctgaatcaatgga 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1979 gettttegtgagetegtetetgatetegegeaagagtgacacacagggtgtteaaagaege 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 ttttattttgattttttttttttttattcgcgcgtaggttaagttgttgaattaatgga 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        979 aagtttttagaaagggtaggaggtcggttttcgaggtttttatttgaagtgag-atgtta 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2099 tggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctctctccc 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1398 gcgg 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2159 gcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC98177 standard; cDNA; 859 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC98177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; nephrotropic; anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                             WO200055351-A1
                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                          21-SEP-2000
                                                                                                                                                                                                                                     12-MAR-1999;
colon cancer associated gene sequences, referred to as colon cancer
                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB53420
                                                                                                                              Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtttttcgtgagttcgtttttgatttcgcgtaagagtgatatataggtgtttaaagacgt 1277
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                                                                                                                                                                                                                                              9905-0124270
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AA AAC97991 to AAC98763 encode the human colon cancer associated proteins, AA AAC97991 to AAC98763 encode the human colon cancer antigens, given in AAB53234 to AAB54006. The CC called human colon cancer antigens can have cytostatic, cardioactive, muscular; CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, cc can be used in gene therapy. The colon cancer antigen polynucleotides, and be used in disposits of the proteins are useful for the prevention, cc crosses and antibodies to the proteins are useful for the prevention, cc chromosome identification, and as hybridisation probes. The proteins cc chromosome identification, and as hybridisation probes. The proteins cc chromosome identification, and as hybridisation probes. The proteins cc gystem disorders, muscular disorders, reproductive disorders, immune cc gastrointestinal disorders, wounds, renal disorders, infectious gystem disorders, and cardiovascular disorders. AAC98772 and CAAB54007 represent sequences used in the exemplification of the present constants.
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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1955 ottoccatcotcgaccaccggggottttcgtgagotcgtotctgatctcgcgcaagag 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2015 tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2135 ccaggcggagctgcctcttctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 ggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccctggctgc 198
                                                                                                                                                                                                                                                                                                                                                    AAZ88700 standard; DNA; 266 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 cgtccgcccacgcgtccgaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 78
                                                                                                                                                                                                                                                                                          11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                          AAZ88700;
                                                                                                                                                                                                                                                                                                                                                                                                                          199 ccaggcggagctgcctcttctcccgcgg 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 138
                                                                                                                                                                                                                     cancer chemotherapy; ss.
                                                                                                                                                                                                                                  p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                             Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                          Homo sapiens
                                                                                                                                           protein_bind
                                                                                     DE19847779-C1.
 16-OCT-1998;
                                                           03-FEB-2000
                              16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
      98DE-1047779.
                                   98DE-1047779.
                                                                                                                                                                Location/Qualifiers
                                                                                                                      /bound_moiety= p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 190.4; DB 21; Length 859; Pred. No. 5.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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WPI; 2000-628395/60.
                           Dean NM,
                                           (ISIS-) ISIS PHARM INC.
                                                                                        10-APR-2000; 2000WO-US09540
                                                                      12-APR-1999;
                                                                                                                      19-OCT-2000.
                                                                                                                                            WO200061150-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                            Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis; Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                 DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                             06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                        AAC61798 standard; DNA; 2551 BP;
                                                                                                                                                                                                                                                                                                                                             AAC61798;
                                                                                                                                                                                                                                                                                                                                                                                                                    2333 9c9g9g9g9g9gagagcctgcagccttcagaacagatat 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2213 aagotttagggttggtggagggggaccccggttggagaggagggggaactcctggacaa 2272
                                                                                                                                                                                                                                                                                                                                                                                                         226 gcggggggggggagagagcctgcagccttcagaacagatat 266
                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron I which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 aagetttagggtegetggaggggaeeeeggttggagaggaggageggaaeteetggaeaa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substances potentially useful for cancer chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel receptor DNA useful for identifying apoptosis-modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-162245/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krammer P, Mueller-Schilling M, Oren M;
                                                                                                                                                                                                                                                                                                                                                                                           σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                     Marcusson EG;
                                                                9908-0290640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                              'product= "Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%; Score 161; DB 21;
100.0%; Pred. No. 3.3e-34;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 266;
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DXX
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AAQ93879
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                             (LXRB-) LXR BIOTECHNOLOGY INC.
                                                                   15-NOV-1993;
                                                                                               15-NOV-1994;
                                                                                                                             26-MAY-1995.
                                                                                                                                                          WO9513701-A.
                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                    s1g_peptide
                                                                                                                                                                                                                                                                                                                Fas-delta-TM; transmembrane deletion; apoptosis; antibody; adoptive immunotherapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Fas-delta-TM cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ93879 standard; cDNA; 2471 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2128 tggctgcccaggcggagctgcctcttctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2068 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2008 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 tygctycccagycygagctycctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region, translational start site, translational termination region or 3'-untranslated region of nucleic acid molecules encoding Fas, Fa expression of Fas, Fast or Fap-1 (Fas associated protein 1, protein tyrosine expression of Fas, Fast or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 gtgaettggetggageeteaggggegggeactggeaeggaacacaceetgaggeeageee 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 71-73; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                           93US-0152443
                                                                                        94WO-US13173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                              /*tag= b
243..1136
                                                                                                                                                                                                                          /*tag= a
195..242
                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                        Location/Qualifiers
Shapiro JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%; Score 155;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. Insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig.3-1 to 3-4; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2094 ggcactggcacggaacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-200120/26.
                                                                                                                                                                                                                                                                                                             Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX24878 standard; DNA; 2471 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2154 ctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                    Soluble Fas receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ctcccgcgg 129
                                                                                                                                                                                                                                                                            Mammalia.
                                                                                                                                                                                               sig_peptide
                                                                                                                  polyA_signal
                                                                                                                                           polyA_signal
                                                                                                                                                                   mat_peptide
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  17-JUL-1997;
                          16-JUL-1998;
                                                                              W09903999-A1
                                                     28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 4.6%; Score 129; DB 16;
Similarity 100.0%; Pred. No. 9e-25;
29; Conservative 0; Mismatches 0;
                             98WO-US14771.
                                                                                                                                                                      /*tag= b
243..1136
                                                                                                                                                                                                /transl_except= (pos:519..521, 195..242
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                     /*tag= 0
2455..2460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                    aa:Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2471;
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CC (see AAW98070). The invention provides a method for inhibiting a CC (see AAW98070). The invention provides a method for inhibiting a CC proinflammatory response in a cell mixture by administering an CC immunosuppressive agent which inhibits the proinflammatory activity (CC immunosuppressive agent which inhibits the proinflammatory activity (CC imflammatory activity). In some embodiments, FasL is coadministered (CC in vivo. Suitable immunosuppressive agent, and the cell mixture comprises (CC in vivo. Suitable immunosuppressive agents include antisense (CC in vivo. Suitable immunosuppressive agents include antisense (CC in vivo. Suitable immunosuppressive agents include antisense (CC enceptors, ribozymes that inhibit the endogenous expression of (CC receptors, ribozymes that inhibit the endogenous expression of (CC endogenous expression of transforming growth factor (TGF)-beta, cc and polynucleotides coding for an immunosuppressive agent such as (CC endogenous expression of transforming growth factor (TGF)-beta, compared the method can be used for treating diseases associated (CC with an undesired FasL-mediated proinflammatory response, e.g. (CC systemic lupus erythematosus, rheumatoid arthritis and psoriasis. (CC condulate FasL stimulation of a proinflammatory response.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
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AAQ29959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen J, Nabel GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW98070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2094 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
                                                                                                                                                                                                                                                                                    AAQ29959 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                               2154 ctcccgcgg 2162
                                                                                                                                                                                                                 12-MAR-1993 (first entry)
                                                                                                                                      Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss
                                                                                                                                                                              Human cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                              121
           mat_peptide
                                                 sig_peptide
                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                              ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.6%; Score 129; DB 20
Similarity 100.0%; Pred. No. 9e-25;
29; Conservative 0; Mismatches
                   /*tag= a
243..1199
                                                     Location/Qualifiers 195..242
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Best Local
                  19-FEB-1996 (first entry)
                                           AAQ95297;
                                                          AAQ95297 standard; cDNA; 2534 BP.
                                                                                                                                                                                                                                                                                                          A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-Ab. The cells were then suspended in buffer containing murine anti-ras antibodies. The Fas-expressing cells adhered with goat anti-mouse Extrachromosomal DNA was prepared from adhered to the plates. transform E.coli VM100 cells. A 520bg XhoI-BamHI fragment from a longest cDNA clone (pF3) was used to screen the KT-3 cDNA library. The to a 335 amino acid pre-protein and a 319 amino acid mature protein
                                                                                                                                 2154 ctcccgcgg 2162
                                                                                                                                                         2094 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                 2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
                                                                                                              121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                   Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monocional antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 1 and 2; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-358914/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Itoh N, Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-1992;
                                                                                                                                                                                     1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg
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                                                                                                                                               ggcactggcacggaacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
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                                                                                                                                                                                                                                        Conservative
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2352..2357
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2518..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= Fas_antigen
1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '*tag=
                                                                                                                                                                                                                                                  100.0%;
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Synthetic
                                                                    06-SEP-1996
                                                                                          AAT16303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP07115988-A.
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wes 129; Conserv
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                                                                 (first entry)
                                                                                                                                                                                                                                                                                      Conservative
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243..1199
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Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
                                                                                      hFas coding sequence from plasmid pCEV4/hFas.
                                                                                                                                                                                                                                                      AAT16303 standard; cDNA; 2534 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2034 gacgettetggggagtgagggaageggtttaeggagtgaettggetggageeteaggggeg 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody production; diseases; treatment; prevention; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pF58 contg. human Fas cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99cact9gcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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100.0%; Pred. No. 9.2e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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sig_peptide
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06-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-1995;
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                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                 This sequence represents the coding sequence for the human Fas antigen is contained within the plasmid pCEV4/hFas. The soluble Fas antigen is contained within the plasmid pCEV4/hFas. The kit is for the representation of the immunoassay kit of the invention. The kit is for the included in the immunoassay kit of the invention immobilised anti-soluble Fas antigen encoded included in the fas antigen and contains an immobilised anti-soluble Fas antigen encoded assay of soluble Fas antigen and as the standard soluble Fas antigen encoded in the sequence. The assay is simple and has high accuracy, high sequence is capable of assaying a number of different specimens by this sequence is capable of assaying a number of different specimens sensitivity, and the immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmine diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-087635/09.
                                                                  AAV32993
                                                                                                                                                                                                                                                                                                                                                                                                                                                             systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;
                                                                                                                                                                                                             2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
                                                                                                                                                                   2094 ggcactggcacggaacacaccctgaggccagcctggctgcccaggcggagctgctctt 2153
                                                                                                                           2154 ctcccgcgg 2162
                                                            AAV32993 standard; cDNA; 2534 BP
                                                                                                                121 ctcccgcgg 129
                                                                                                                                                         61 ggcactggcacggaacacaccctgaggccagccctggchgcccaggcggagctgcctctt 120
                                        AAV32993;
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                     18-NOV-1998
Fas cDNA.
                                                                                     12
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Noguchi J, Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= ras antigen
195..242
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243..1
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195..1201
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94JP-0154706.
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                           (first entry)
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100.0%; Pred. No. 9.2e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS INNOVATION LTD.
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                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                 pisclosure; Fig 10; 71pp; English.
                                                                           Best Local Similarity
Matches 129; Conserve
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-456867/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97GB-0003276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-GB00485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Fas protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243. 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= C
1831..1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195..242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                              100.08; ]
                                                                                               Mismatches
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SXXCCCCCCCXXXX PPPXX PXXX PXX PXX PXX PPXX PPX

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The present sequence represents a ras cuma sequence used in the method of the invention. The method is concerned with reducing TRX) method of the invention. The method is concerned with reducing TRX) comparison to the invention. The method is concerned with reducing TRX) comparison to the invention of activated Fas-Expressing comparison to fan agent (e.g. a cells in an immune cell toppulation which also comparison to the serior of activated CC (rash) expressing activated CD4+ cells. In the mount of an agent the comparison of activated CC (ratheristic composition for the serior population protein) which would interfer with the serior of activated CC (ratheristic compositions) and Fasi. Therefore, the method is cuseful for composition of activated CC (ratheristic composition for the serior population of activated CC (ratheristic compositions) and Fasi. The reduce deplation of activated CC (ratheristic compositions) and fasi. The reduce deplation of the composition of comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ras protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL; Fas protein; CD8+ T-lymphocyte; human immunodeficiency virus; HIV; CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL; sinian immunodeficiency virus; SIV; cytotoxic T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency Reducing CD8+ lymphocyte apoptosis to treat e.g. with Fas-ligand Reducing CD8+ lymphocyte apoptosis to treat e.g. with Fas-ligand diseases - by interfering with interaction of Fas with HIV diseases - by interfering with interaction of Fas with HIV expressed on activated CD4+ cells, e.g. cells infected with HIV expressed on activated CD4+ cells,
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
4.6%; Score 129; DB 19;
100.0%; Pred. NO. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                      DB 19; Length 2534;
                                                                                                                                                                                                                                                                                        Indels 0;
                                                                                                                                                                                                                                                                                                                          Gaps
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Дb

2154 ctcccgcgg 2162

B

2094 99cact99cac99aacacaccct9a99cca9ccct99ct9ccca99cg9a9ctgcctctt 2153

1 9acgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60

61 gcactggcacggaacacacctgaggccagccctggctgcccaggcggagctgcctctt 120

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The present sequence was used in the development of novel Fas region lacking one or more amino acid residues in the region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine region from used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, such as hepatitis, influenza and HIV, by modulating apoptosis of the region of the coding DNA in gene therapy to treat a range of diseases, such as hepatitis, influenza and HIV, by modulating apoptosis of
Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                                                                  Disclosure; Fig 1-2; 102pp; Japanese.
                                                                                                                                                                                  Fas antigen derivative containing modified extracellular region - f...., antigenicity, promotes apoptosis and is useful in treatment
                                                                                                                                                                                                                                                   P-PSDB; AAW50289.
                                                                                                                                                                                                                                                            WPI; 1997-558981/51.
                                                                                                                                                                                                                                                                                        Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                 (MOCH ) MOCHIDA PHARM CO LTD.
(OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                            02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                             WO9742319-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis modulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Fas antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV07002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV07002 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                Nakamura N;
                                                                                                                                                                                                                                                                                                                                    96JP-0135760.
                                                                                                                                                                                                                                                                                                                                                         97WO-JP01502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
243..1199
                                                                                                                                                                                                                                                                                                                                                                                                                    /product= Fas_antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 242
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Query Match
2114 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 2173
                                                                                                                                        Shuttle vector padbel.CMVDys (AAT27558) comprises the adenovirus is elements needed for replication and virion encapsidation but sis deleted of all viral genes. It carries a mouse dystrophin virus that supplies the sequences needed for a productive viral adenovirus is produced that disabled packaging function. Recombinant transgene into the host cells and the ability to stably integrate the to transfer the dystrophin gene for use in muscular dystrophy gene therapy.
                                                                                                             Sequence 19307 BP; 4816 A; 4393 C; 4056 G; 6042 T; 0 other;
                                                                                                                                                                                                                                                                                                             Example 9; Fig 12A-12P; 149pp; English.
                                                                                                                                                                                                                                                                                                                     Recombinant adenovirus produced from shuttle vector and helper virus transgene(s) to target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen S, Fisher KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09613597-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenovirus type 5; Ad5; vector; gene therapy; gene transfer;
helper virus; dystrophin; muscular dystrophy; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.2%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shuttle vector pAdDel.CMVDys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT27558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT27558 standard; cDNA; 19307 BP.
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2154 ctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2094 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2034 gacycttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gacgcttctggggagtcagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0331381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US14017.
                                                      2.2%; Score 63.6; DB 17; Length 19307;
                                                                                                                                                                                                                                                                                                                                                                                                                          Weitzman M,
                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson Jм;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 127.4; DB 1
Pred. No. 2.5e-24;
0; Mismatches 1
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AAT27557/c
ID AAT275
AC AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16108 gctcgagaagtactagtggccacgtgggccgtgcaccttaagcttggcactggccgtcgt 16167
                                                2174 gctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggagg 2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16168 tttacaacgtcgtgactgggaa 16189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              755//C
AAT27557 standard; cDNA; 9972 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT27557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shuttle vector padDel.CBCFTRZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; cystic fibrosis transmembrane conductance regulator; helper virus; cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CETR; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_unit
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                                                                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                            09-MAY-1996.
                                                                                                                                                                                                                                W09613597-A2.
                                                                                                                                                    27-OCT-1995;
                                   Chen S, Fisher KJ, Weitzman M,
                                                                    (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                 28-OCT-1994;
WPI; 1996-251463/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_type= INVERTED inverted terminal repeat" /note= 3, adenovirus inverted complement (3887..3684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (3652..3073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function= CFTR gene
complement (9241..8684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8622..4065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "5' adenovirus înverted terminal repeat"
complement (9374..9360)
/*tao= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (9611..9254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= CMV enhancer/beta actin promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function= packaging sequence PAC I complement (9353..9340)
                                                                                                                                                                                                                                                                                                                                                                              /function= packaging sequence PAC III complement (9301..9288)
                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= packaging sequence PAC II
complement (9311..9298)
                                                                                                                                                                                                                                                                                                                  /function packaging sequence PAC IV complement (9276..9263)
                                                                                                                          94US-0331381.
                                                                                                                                                               95WO-US14017.
                                                                                                                                                                                                                                                                                 /function= packaging sequence PAC V
                                                                    Wilson | JM;
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80
                                                                                                                                                                        Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant adenovirus produced from shuttle vector and helper virus - has crippled packaging function, useful for delivering transgene(s) to target cells
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cis elements needed for replication and virion encapsidation but is deleted of all viral genes. It carries a CFTW gene under the control of a chimeric CMV enhancer/chicken beta-actin promoter. It is used with a helper virus that supplies the gequences needed for a productive viral infection but which has disabled packaging function. It is used with a helper virus that supplies to haracterized by high titer a productive viral infection but which has disabled packaging function. It is used with a host cell and the ability to stably integrate the ransgene delivery to host cells and the ability to stably integrate the transgene into the host cell chromosome. Such a vector can be used to transfer the CFTR gene for use in cystic fibrosis gene therapy.
                                                                                                                                                                                                                                                                                                                                Matches
search completed: September 7, 2002, 18:43:03
gob time: 30077 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 7A-7H; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9972 BP; 2581 A; 2362 C; 2245 G; 2784 T; 0 other;
                                                                                                                                                                                                                                                 2175 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggaggg 2234
                                                                                                                                                                        2920 CTCGAGAAGTACTAGTGGCCACGTGGGCCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                                                 2235 ggaccccqgttggagagagga 2255
                                                                                                                                                                                                                                                                                                                             y Match 2.2%;
Local Similarity 65.2%;
Local Similarity 65.2%;
les 92; Conservative
                                                                                                2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                           score 62.6; DB 17
pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 9972;
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## us-09-834-291-4.rnpm

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            September 7, 2002, 22:33:42; Search time 13836.9 Seconds (without alignments) 4420.187 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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2827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tgaggactctcaggaatatg.....tggctaatcaaagagacgtg 2827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21979536 seqs, 10817449327 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/2/pna/F
2: /cgn2_6/ptodata/2/pna/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pred. No. is the number of results predicted by chance to have a pred. No. is the number of the score of the result being printed, score greater than or equal to the score of their bution. and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                             2370.4
2346.6
1714.4
1714.4
1372.8
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424.2
424.2
319.6
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296.8
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. '.cgn2_6/ptodata/2/pna/US6011_COMB.seq:*

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. '.cgn2_6/ptodata/2/pna/US6035_COMB.seq:*

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. '.cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

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/cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
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Sequence 4 Application US/09834291
APPLICANT Krammer, Peter
APPLICANT Krammer, Peter
APPLICANT Krammer, Peter
APPLICANT Wuller Schilling, Martina
FILE OF INVENTION: D53 Binding Areas
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: D51/DE99/03343
PRIOR FILING DATE: 1998-10-16
SOFTWARRE. DATE: 1998-10-16
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FILE OF INVENTION Eric	
APPLICANT: MOTTIS, David	-399cgltccccagcg 1947
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; ORGANISM: HOMO Sapiens
US-09-834-291-1
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
FILE REFERENCE: 4121-122
CURRENT APPLICATION: p53 Binding Areas
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 1990-10-16
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: DE 198 47 779.1
SOFTWARF: P54CON 100S: 32
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SOFTWARF: P54CON 100S: 32
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Best Local Similarity 83.0.
Matches 2795; Conservative
                                                                                                 241 ctaagattatttgaccatgaaacatatgtctccccacaaagcacatattcctatctcctt 300
                                                                                                           241 ctaagattatttgaccatgaaacatatgtctccccacaaagcacatattcctatctcctt 300
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                                                                                                                                                                                                                   61 tttccccagaacaccagcattcattaggtgttcattcaatagattcttcaaaggattcca 120
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gaaagaattacaagatttttttttaaagaaaattggccag gaaagaattacaagatttttttttaaagaaaattggccag	
1261 catgctaaactacctaagagctatctaccgttccaaagcairugugugugugugugugugugugugugugugugugugug	
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901 acaagcctatcaacacctacaagactggtggtaagtgcaggtgacagatgcaaaacac 	p 24
841 ggctggcacgcccaggfcttactactagcagtctactgaaaaggtggaacagg 9	da Ao
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781   Teccatectecttateceaettettettegtgtetattagatgeteagagtgytytettettegtgtetattagattgeteagagtgytytettettegtgtetattagattgeteagagtgytgtgcaeaa 84	Qy
721 attttggaatagttttaggatttcaaaaaatttgcagagataatacagagaatgccaa	Qy
ccttccttcttttcacatttttttatttaaatgaacttt	dg VQ
	рb
ctttccccttttttctctctccct	Qy D
41 cacatatgtgagttgctggcttataattcacactcaagagatactgattttgtcaattgt 60	Qy Db
81 taagtttaataatcactcatctcactgggctataatgataagtattaagtaag	Qy
gottaagottttttggctacattttttatttgtaaa -gottaagottttttggctacattttttatttgtaaa -gottaagotttttggctacatttaagtaaggaagat	рb

Db 1500 cagagocttatggcgcaacatcgtacttttcatatggttaactgtcaattggttaactgtcaattggttaactgtcaattggttaactgtcaattggttaactgtcaattggcagccaagtcaaattgcagtcaattggcagccaagtcaattggcagcagcagcagtcaattggcagcagcagcagtcaattggcagtcaattagcagcagcagcagcagtcaattggcagcagcagcagcagtcaattggcagcagcagcagcagcagcagtcaattggcagcagcagcagcagcagtcaattagcagcaggtccattcactgtaaccaggagtcgagtcaattagcagcaggtcaagttggagcaggtcaattagcaggtcaagttggagcaggtcaagttggagcaggtcaagttggagcaggtcaagttggagcaggtcaagttggagcaggtcaagttggagcaggtcaagttggagcaggtcaagttggagcaggtaggaggaggaggaggaggaggaggaggaggaggagg
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; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-665-615B-94
                                                             Matches 1715;
                                                                                   Query Match
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                                                                                                                                                                                          APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Myatt, Jacqueline
FILE PREFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
PRIOR APPLICATION NUMBER: US 09/290,640
NUMBER OF SEQ ID NOS: 179
NUMBER OF SEQ ID NOS: 179
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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RESULT 6 US-09-802-669-94 US-09-802-669-94 Sequence 94, Application US/09802669 Sequence 94, Application US/09802669 GENERAL INFORMATION: APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G. APPLICANT: Myatt, Jacqueline APPLICANT: Wyatt, Jacqueline APPLICANTION UNMAER: US/09/802,669 CURRENT FILING DATE: 109-0-18 PRIOR APPLICANTION UNMAER: US 09/665,615 PRIOR PILING DATE: 2000-09-18 PRIOR PILING DATE: 1999-04-12 PRIOR PILING DATE: 1999-18 PRIOR P	y 1587 acaacatygacagccagtcaaatgccccgcaagtctttctctgagtgactccagcaatt 1646 1141 acaacatygacagcccggtcaaatgccccggcaagtctttctcttgagtgactccagcaatt 1200 1141 acaacatygacagcccggtcaaatgccccggcaagtctttctcttgagtgactccagcaatt 1200 1141 acaacatygacagcccggtcaaatgccccggcaagtctttctcttgagtgactccagcaatt 1200 1141 acaacatygacagcccggtcaccaggcagcagcatttaggagctccgattcttctctttaaga 1706 1201 agccaaggtctctgagccaggaggagcctttaggaggcctctgaggaggcgggaggaggcgggaggaggcgggaggaggcgggagga
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                                   COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/377,522
CTICKY-TERMINED: 20-TAN-1995
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                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                    APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, William J.
APPLICANT: Zhou, Tong
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                 STREET: P.O. Bo
CITY: Houston
STATE: Texas
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ZIP: 77210
                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1887 ccgcgcgcaggccaagttgctgaatcaatggagccctccccaacccgggcgttccccagc 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1321 totogaggtootcacotgaagtgagcatgocagccactgoaggaacgcocogggacagga 1380
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                                                                                                                                                                                                               P.O. Box 4433
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                      20-JAN-1995
N: 435
                                                                                                                   Floppy disk
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1487 gggccctcccttttcagagccctatggcgcaacatctgtactttttcatatggttaactg 1546
                        US-08-377-522-1
                                                                             1367 ggccaggaaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg 1426
                                                                                                                        Query Match
48.6%; Score 1372.8; DB 7; Length 1608;
Best Local Similarity 99.4%; Pred. No. 2.4e-287;
Matches 1388; Conservative 0; Mismatches 7; Indels 1;
                                                                  607 GGCCAGGAAATAATGAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGG 666
                                                                                                            1187 tgtccagtctggaactgcatccaaattcaggttcagtaatgatgtcattatccaaacata 1246
                                                                                                                                                                                                                                                        1127 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 1186
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SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
                                                                                                                                                                                                                                                                                                                                                                          127 AAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                 887 aaggtggaacagagacaagcctatcaacacctacaagactggtggtaagtgcagtgacag 946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sertich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512,418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                 CCAAACAGGCTCCAGAAGAAAATGTCAACTGAGGAAGGCAAGGCTGAAGGATGAACAGTGGGC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1467..1496
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DEDNESS: single
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                                                                                                                                                                                                                                                           967
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                                                                                                                                                                        2147 gcctcttctcccgcgg 2162
                                                                                                                                                              1386
                                                         STATE: TX
ZIP: 77071
COMPUTER READABLE FORM: floppy
MEDIUM TYPE: 3.5 inch floppy
         FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                  SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  STREET: 8011 CITY: Houston
                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                             ADDRESSEE:
                            APPLICATION NUMBER: US/08/377,522C
                                                                                                                                              œ
     APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                              GCCTCTTCTCCCGCGG 1401
                                                                                        E: Benjamin Aaron Adler, Ph.D., J.D
8011 Candle Lane
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; PUBLICATION INFORMATION: US-08-377-522C-1
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TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: IN ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: placental
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIXI; EMBL-SP6/T7
LIBRARY: (FIXI; EXZ, FIX3; EMBL1, EMBL2, EMBL3
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
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                                                                                                                                                 1127 ttgcagagtgaggtgcagagctttggtggacgatgccaaaggaatactgaaacctttagtg 1186
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                                                                                                     1187 tgtccagtctggaactgcatccaaattcaggttcagtaatgatgtcattatccaaacata 1246
                                                         1247 cottotgtaaaattoatgotaaactacotaagagotatotacogttocaaagcaatagtg 1306
                                                                                                                                     307 TAAGCAAAGGGTTATTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGG 366
487 CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG 546
                                                                                           427 TGTCCAGTCTGGAACTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATA 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.6%; Score 1372.8; DB 7; Length 1608; 99.4%; pred. No. 2.4e-287;
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Sequence 1, Application US/08377522D GENERAL INFORMATION:
                                         COMPUTER READABLE FORM:
                                                                                                                         APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              1386 GCCTCTTCTCCCGCGG 1401
                                                                                                                                                                                                                                                                                               2147 gcctcttctcccgcgg 2162
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                                                                                                    E: Benjamin Aaron Adler, Ph.D., J.D.
8011 Candle Lane
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NAME: Benjamin Aaron Adler, Ph.D., J.D.

REGISTRATION NUMBER: 35 423

REFERENCE, DOCKET NUMBER: D5919

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 777-2321

FELEPAX: (713) 777-6908

INFORMATION FOR SEQ ID NO: 1:
             1127 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                     1007 ccaaacaggctccagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggc 1066
367 TTGCAGAGTGAGGTGCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTG 426
                                                                                                            247 CCAAACAGGCTCCAGAAGAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGC 306
                                                                                                                                                                  187 ATGCAAAACACAGGGTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGC 246
                                                                                                                                                                                947 atgcaaaacacagggtgatggaaagccctcaggagggtaacctaacctagatttgagggc 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: CHAPOTHETICAL: NC ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                            827 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
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LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMB
                                                                                                                                                                                                                                                                             67 GAGTGTGTGCACAAGGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    7 ACAGAGATGCCCTATACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCA 66
                                                                                                                                                                                                                                                                                                                                                                                                       / Match 48.6%; Score 1372.8; DB 7; Length 1608; Local Similarity 99.4%; Pred. No. 2.4e-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Januar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1608 bp
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                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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US-08-377-522D-1

ADDRESSEE: Ben STREET: 8011 C: CITY: Houston STATE: TX ZIP: 77071 COUNTR: USA

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US-60-324-185-29531
Sequence 29531, Application US/60324185
GENERAL INFORMATION:
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                                                         1266 GTTCAAAGACGCTTCTGGGGAGTGAGGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTC 1325
                         1386 GCCTCTTCTCCCGCGG 1401
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                                                                                                                                            GAACTACAGCAGAAGCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAA 1026
                                                                                                                           GTGAG-ATGCCAGCCACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAA 1085
                                                                                                                                gcctcttctcccgcgg 2162
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 415714.1
US-60-324-185-29531
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LENGTH: 3814
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APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
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CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1506 ccctatggcgcaacatctgtactttttcatatggttaactgtccattccaggaacgtctg 1565
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les 717; Conserva
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                                                                                                                                                                                                                                                                                               241
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                                                                                          1986 gtgagotogtototgatotogogoaagagtgacacacaggtgttcaaagacgcttotggg 2045
         2105 ggaacacaccctgaggccagcctggctgcccaggcggagctgcctcttctcccgcgg 2162
                                                 421 ctgacttotococtocotaccogogogoggocaagttgotgaatcaatggagecetec 480
                                                                                                                        481 ccaaccegggcgttccccagcgaggcttccttcccatccttgaccaccggggcttttc 540
                                                                                541 gtgagetegtetetgatetegegeaagagtgacacacaggtgtteaaagaegettetggg 600
                                        gagotocattotoottoaagacotococaacttocoaggttgaactacagcagaagcott 300
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ggaacacaccctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 718
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LENGTH: 720
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-2
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: U5/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOS: 32
                  2813 aatcaaagagacgtg 2827
                                                         2753 aaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 2812
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706 aatcaaagagacgtg 720
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                                          646 aaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 705
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                                                                                                    586 tgctggggttggtggtactcgttcccaccgcacagaacccggcgcctattattggccaag 645
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                                                                                                                                                               526 ctctttcttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcc 585
                                                                                                                                                                                                                            466 ctotttaagactgtaagtogotgcotgagtggtttcattttgtttttgtttttctgccctt 525
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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99.7%;
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Pred. No. 3.6e-122;
0; Mismatches 2; Indels 0;
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Sequence 574, Application US/09524038
GENERAL INFORMATION:
APPLICANT: DIMENAC, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee w.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 780CIP
CURRENT APPLICATION NUMBER: US/09/524,038
CURRENT FILING DATE: 2000-03-13
EARLIER APPLICATION NUMBER: 09/404,284
EARLIER FILING DATE: 1999-09-21
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Best Local
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TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-780
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     29 GGCACGGGA 21
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; ORGANISM: Homo sapiens US-09-524-038-674
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SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 674
                                                             US-09-306-350A-14682
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Best Local Similarity 99.3%;
                                                                                                                                                                                                                                                                             Sequence 14682, Application US/09306350A GENERAL INFORMATION:
                                                                                                                                  APPLICANT: Jones, Lee W.

APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various cDNA Libraries
TILE REFERENCE: 20411-776
CURRENT APPLICATION NUMBER: US/09/306,350A
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
                                                                                                              SOFTWARE: pt_CT_1 Version 1.1
SEQ ID NO 14682
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                        Query Match
Matches
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                                                                          ORGANISM: Homo sapiens
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            / Match 11.3%;
Local Similarity 96.3%;
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 Mismatches

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Pred. No. 1.7e-81;

 Mismatches

              score 319.6; DB 17; pred. No. 9.1e-59;
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                             Length 458;
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US-09-909-629-14682/c
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SEQ ID NO 14682
                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various cDNA Libraries FILE REFERENCE: 20411-776
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/909,629
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 41304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1141 gcagagcttggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctggaa 1200
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                                                                                                                                                                                                                                                                                               LENGTH: 458
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                                              1021 gaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggctaagcaaagggtta 1080
          1141 gcagagettggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctggaa 1200
                                                                                                                                            Match 11.3%; Score 319.6; DB 34; Length 458; Local Similarity 96.3%; Pred. No. 9.1e-59;
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                                                                                                                                                                                               391; Conservative
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Labat, Ivan
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 Mismatches

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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB:seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

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6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-10-035-832-1262
US-10-11-154-674
US-10-11-154-674
US-10-11-364-477
US-10-143-906-21
PCT-US02-10824-85
PCT-US02-25766-394
US-10-035-832-1263
US-10-035-832-1253
US-10-035-832-1259
US-10-13-872-796
US-10-13-872-796
US-10-13-872-1669
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US-10-027-632-134015
US-10-027-632-134015
US-10-027-632-134015
US-10-027-632-134015
US-10-175-523-103
US-10-027-632-253750
US-10-027-632-253750
US-10-027-632-253750
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                                                                                                                                                     Sequence 1262, Ap
Sequence 674, App
Sequence 477, Appl
Sequence 21, Appl
Sequence 85, Appl
Sequence 9394, Ap
Sequence 1263, Ap
Sequence 1263, Ap
Sequence 1259, Ap
Sequence 1359, Ap
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                           134015,
134016,
10281, A
10281, A
103, App
103, App
2303, App
2303, App
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91808, A
         253751,
64316, /
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OY	US-11188831	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Query Match Bast Local Similarity B7.1%; Pred. No. 0; Best Local Similarity B7.1%; Pred. No. 0; Bast Local Similarity B7.1%; Pred. No. 0; Bast Local Similarity B7.1%; Pred. No. 0; B111	SULT 1 1-0-035-832-1262 Sequence 1262, Application US/10035832 Sequence 1262, Application US/10035832 Sequence 1262, Application US/10035832 Sequence 1262, Application US/10035832 AppLICANT: Morris, David AppLICANT: Engelhard, Eric AppLICANT: Engelhard, Eric AppLICANT: MOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CURRENT FILING DATE: 2002-07-22 CURRENT FILING DATE: 2002-07-22 CURRENT FILING DATE: 2001-03-22 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-2 NUMBER OF SEQ ID NOS: 1613 SOFTWARE: PATENTIN VERSION 3.1 SEQ ID NO 1262 LENGTH: 45121 TYPE: DNA ORGANISM: Homo Sapiens	26 55.2 2.0 443 7 US-10-027-632-64317 27 55.2 2.0 443 7 US-10-027-632-296990 28 55.2 2.0 443 7 US-10-027-632-296991 28 55.2 2.0 143 7 US-10-027-632-296991 29 54.8 1.9 11091139 5 US-09-611-352B-1 30 54.8 1.9 1109139 7 US-10-027-632-103140 31 54.6 1.9 2501 7 US-10-027-632-1103140 32 54.6 1.9 48763 1 US-10-027-632-71673 34 54.4 1.9 1076 6 US-10-027-632-71673 35 54.4 1.9 44990 6 US-10-035-832-1229 36 54.4 1.9 44990 6 US-10-035-832-1229 37 54.2 1.9 113585 6 US-10-035-832-1229 38 54.3 1.9 375 0 US-10-027-632-111688 39 54 1.9 27827 6 US-10-037-832-1328 39 54 1.9 375 1 PCT-US02-09239-331 40 53.8 1.9 375 1 PCT-US02-09188-1404 41 53.8 1.9 375 1 PCT-US02-09257-784 42 53.8 1.9 375 1 PCT-US02-09257-784 43 53.8 1.9 375 1 PCT-US02-09257-784 44 53.8 1.9 375 1 PCT-US02-09257-786
ength 45121;  dels 393; Gaps  attgcccaaactgt 60                               tcaaaggattcca 120	CANCER	Sequence 64317, A Sequence 296990, Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 103140, Sequence 103140, Sequence 17673, A Sequence 1226, App Sequence 1229, App Sequence 1217, App Sequence 111668, Sequence 1328, Ap Sequence 3138, Ap Sequence 31402, Ap Sequence 1402, Ap Sequence 1402, Ap Sequence 1404, Ap Sequence 1404, Ap Sequence 1784, App Sequence 1784, App

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gttagctttgttttcctcttgagaaataaaactaag	Db 10454 ctggaggacttg	Фу 2210	Db 10394 gttggagactgg	2210	10334 gggattgcggc	Oy 2210	2188	10214 aacaaccatgc	Qy 2188	10154 gggttggtgga	Qy 2161 g	Db 10094 gcacggaacac	cacggaaca	1003	2041 ctgggatg	01	9914 cctcccaac	ctccccaac	9854 tcaccctgac	1861 tcaccctgac	97	/34 gcctttaga 801 cacttaga	b 174	9674 gctctgagc	Qy 1681 gctctgagc	Db 9614 tctttctct	ctttctct	9554 gtctgtgag	1561 atatatasa	94 cagageeet	9434 gcttaagtt	144	
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                                                                                                                                                                                                                                                                                                                      Sequence 674, Application US/10011154 GENERAL INFORMATION:
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TITLE OF INVENTION: From Various Libraries

FILE REFERENCE: 780CIP
FILE REFERENCE: 780CIP
CURRENT APPLICATION NUMBER: US/10/011,154

CURRENT EILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
                                                                                                                                                                                                                                APPLICANT: Drmanac, Radoje T.
APPLICANT: Labbat, Ivan
APPLICANT: Stache-Crain, Bir9
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee W.
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            SEQ ID NO 674
LENGTH: 449
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TYPE: DNA
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; Sequence 477, Application US/10211364
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                                               PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR PRIOR PRICATION NUMBER: 60/225,447
PRIOR PRIOR APPLICATION NUMBER: 60/225,447
PRIOR PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR PILING DATE: 2000-08-14
PRIOR PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/760,486
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 69/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 69/180,628
PRIOR APPLICATION NUMBER: 69/180,628
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CURRENT FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PJZ16C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1920 ccctccccaacccgggcgttccccagcgaggcttcccttcccatcctcctgaccaccgggg 1979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1778 SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 CTCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 TCTGGGGAGTGAGGAAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGCACT 30
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US-10-143-906-21
       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ70C1N
CURRENT APPLICATION NUMBER: US/10/143,906
CURRENT FILING DATE: 2002-05-14
                                                                     OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                 OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
                                                                                             NAME/KEY: misc_feature LOCATION: (704)
                                                                                                                                FEATURE:
                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                      LOCATION: (594
                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (593)
                                                                                                                                                                                                                                             FEATURE:
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LENGTH: 772
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NAME/KEY: misc_feature
LOCATION: (704)
OTHER INFORMATION: n equals a,t,g, or c
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      8.4%;
99.6%;
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Score 237.4; DB 7
Pred. No. 5.1e~41;
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              DB 7;
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         Length 772;
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Sequence 9394, Application PC/TUS0225766
GENERAL INFORMATION:
APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNOER, William E
APPLICANT: FAULK, Ronald
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, IWAO
APPLICANT: YAMAMOTO, Jun
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SOFTWARE: Patentin version 3.1
SEQ ID NO 85
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US02-10824-85
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, Iwa
APPLICANT: WAGA, Iwa
APPLICANT: WAGA, Iwa
APPLICANT: YAMAMOTO, Jun
TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
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Sequence 85, Application PC/TUS0210824
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Prostate Cancer Expression Profiles
FILE REFERENCE: 9U 206 PCT
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/281,732
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
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APPLICANT: Engelhard Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TILE REFERENCE: A-71249/MS/DCF
CURRENT FILING DATE: 2002-07-22
CURRENT FILING DATE: 2002-07-22
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOSTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1263
LENGTH: 2551
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-10-035-832-1263
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SEQ ID NO 9394
LENGTH: 2551
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; Sequence 143, Application US/10007926A
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                       US-10-007-926A-143
                                              RESULT
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PRIOR FILING DATE: 2001-08-14
                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%; Score 155; DB 6; Length 2551; Best Local Similarity 100.0%; Pred. No. 3.1e-23; Matches 155; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                   2128 tggctgcccaggcggagctgcctcttctcccgcgg 2162
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                                                                                                  tggctgcccaggcggagctgcctcttctcccgcgg 155
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100.0%; Pred. No. 3.1e-23;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-053-375B-233
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NGUYEN, CATHERINE APPLICANT: VIENS, PATRICE APPLICANT: FERT, VINCENT
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CURRENT FILING DATE: 2001-12-07
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                                                                                                                                             Query Match 4.6%; Score 129; DB 5; Length 2534; Best Local Similarity 100.0%; Pred. No. 1.1e-17; Matches 129; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/053,375B CURRENT FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid Arrays FILE REFERENCE: CLON-006
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chenchik, Alex APPLICANT: Bibilashvilli, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: tumor necrosis factor receptor superfamily, OTHER INFORMATION: member 6 (TNFRSF6) gene.
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                                                                                                                                                                                                                                                    LENGTH: 2534
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2094 ggcactggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y Match 5.5%; Score 155; DB 7;
Local Similarity 100.0%; Pred. No. 3.1e-23;
hes 155; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
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BIRNBAUM, DANIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2551;
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                                                                                                                                                              0; Gaps
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2154 ctcccgcgg 2162

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CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR ETLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEQ ID NO 1259
                                                                                                                                                                                         Matches 152; Conserv
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-035-832-1259
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                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (55549)..(55568)
OTHER INFORMATION: "n" at positions 55549 thru 55568 can be any base
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (53136)..(53155)
OTHER INFORMATION: "n" at positions 53136 thru 53155 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1259, Application US/10035832 GENERAL INFORMATION:
7799 cagtaaagaagtataagaattttttttaacgaaaattggtcaggaaataatccgtaacaa 7858
                        1330 cacgaaagaattacaagatttttttttaaagaaaattggccaggaaataatgagtaacga 1389
                                                                                 1272 acctaagagctatctaccgttccaaagcaatagtgactttgaacagtgttcacca--gag 1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (50692)..(50711)
OTHER INFORMATION: "n" at positions 50692 thru 50711 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (48271)..(48290)
OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (29253)..(29272)
OTHER INFORMATION: "n" at positions 29253 thru 29272 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (469\overline{8}7)...(47006)
OTHER INFORMATION: "n" at positons 46987 thru 47006 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (46987)...(47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (42691)..(42710)
OTHER INFORMATION: "n" at positions 42691 thru 42710 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (42691)..(42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (31023)..(31239)
OTHER INFORMATION: "n" at |
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                                                                                                                                                                                       Conservative
                                                                                                                                                                                                    2.4%; 63.6%;
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                                                                                                                                                                                    0;
                                                                                                                                                                     Score 68.2; DB 6; Length 55996;
Pred. No. 0.00028;
0; Mismatches 83; Indels 4;
                                                                                                                                                                     4; Gaps
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US-10-113-872-796/c
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: US 60/185,218
PRIOR FILING DATE: US 60/185,218
PRIOR FILING DATE: US 60/185,218
PRIOR FILING DATE: 1099-11-23
                                                                                                                                                           APPLICANT:
APPLICANT:
                  CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                  APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
                                                                                                                                                                                                                                         APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert,
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145670
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                       247 AAGATAGTACAGAAAATTCCCACATACTGCACACCGTTTCCCCCTGTTTTTAACATTTTAT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                757 gagataatacagagaatgcccattataccatccttcttatcccacttctttttgtgtctat 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 tttttttatttaaatgaacttttcattttggaatagttttaggatttcaaaaaatttgca 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7859 aag-gaggaagtaataatgtet-aacacageaggtgagggttttecettttaetgaaaat 7916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                              Vedvick, Thomas S.
                                                                                                                                                                                                                                    Kalos, Michael D.
                                                                                                                                                                                                                  Sleath, Paul R.
                                                                                                                                                                       Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                           Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60.8; DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-10-113-872-796
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Sequence 91808, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION OF SECURITY OF
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APPLICANT:
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Vedvick, Thomas S.
Carter, Darrick
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US-10-027-632-304597
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91808
LENGTH: 542
                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-304597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/185,218
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                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 304597
LENGTH: 542
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ORGANISM: Human
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PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/145,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 1999-09-28
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Local Similarity 79.5%;
es 70; Conservation
                                           757 gagataatacagagaatgcccatatacc 784
                                                                                                                                   Watch 2.1%; Score 59.2; DB 7; Length 542;
Local Similarity 79.5%; Pred. No. 0.0066;
nes 70; Conservative 0; Mismatches 18; Indels
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Db 104 gagataatacaaaagttccttcacacc 131
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Search completed: September 8, 2002, 01:14:46

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1 465.4 16.5 467 9 AA704610 2 438.4 15.5 793 10 B1763679 3 298.4 10.6 603 9 AA058563 4 294.4 10.4 577 9 AA058563 5 286.4 10.1 442 9 AA047220 6 286.4 10.1 547 9 AA047220 7 285.4 10.1 447 9 AA047220 8 276.4 9.8 467 9 AA025418 9 276.4 9.8 467 9 AA025992 8 276.4 9.8 376 10 H86298 10 259 9.2 398 10 H86126 11 254.4 9.0 297 9 AA018441 11 254.4 9.0 297 9 AA018441 12 253.6 9.0 381 10 H86827 13 197 7.0 419 10 R85827 14 185.2 6.6 696 9 AV715411 15 181.8 6.4 828 10 B138027 17 145.6 5.2 1339 10 BG288747	of the score of the of the total score di SUMMARIES	EST:*  1: em_estba:* 2: em_esthum:* 3: em_esthu:* 4: em_estou:* 5: em_estov:* 6: em_estov:* 6: em_esto:* 1: gb_est1:* 1: gb_est2:* 11: gb_htc:* 12: gb_gss:* 13: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_pin:* 16: em_gss_pri:* 17: em_gss_pin:* 18: em_gss_pin:* 19: em_gss_pin:*	ım Match ng first	ው ው	Total number of hits satisfying chosen parameters:	Searched: 13736207 seqs, 6748477542 residues	US-09-834-291-4 score: 2827 store: 1 tgaggactctcaggaatatg	using sw model 7, 2002, 14:51:47 ; Search (without 4508.751	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
AA/04610 ZJ19104.5 B1/3679 603049567 AA058563 zf55b04.s AA05867 zf53903.s AA011028 ze34002.s AA047220 zf49e11.s AA047220 zf49e11.s AA057418 zf59h03.s AA020992 ze65f07.s - H84298 ys99e09.s1 H86126 ys94908.s1 AA018441 ze50a08.s H86254 yt044f01.s1 R85827 yq22910.s1 AV715411 AV715411 B1183827 603083875 AW239285 xb38d02.y BG288747 602385566	e result being prince, distribution. JOURNAL COMMENT Description	RESULT 1 AA704610 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM Chance to have a AUTHORS			40	35 36 37		c 24 time 8462.63 Seconds c 25 alignments) 26 Million cell updates/sec 28 66	18 1 19 20 1 20 1 2 22 2
Email: est@watson.wustr.euc This clone is available royalty-free throug IMAGE Consortium (info@image.llnl.gov) for Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 459. Location/Qualifiers 1. 467 /organism="Homo sapiens" /ob_xref="GDB:1387127" /db_xref="Taxon:9606" /clone="IMAGE:450771" /clone="IMAGE:450771" /sex="male" /sex="male" /lab_host="phi0B (ampicillin resi /lab_host="Phi0B (ampicillin resi /note="Organ: Liver and Spleen; V	White, Y., W WashU-NCI h Unpublished Contact: Wi Washington 4444 Forest Tel: 314 28 Fax: 314 28	AA704610 Zj19h02.sl Soares_fetal_ Zj19h02.sl Soares_fetal_ Clone IMAGE:450771 3', n AA704610 AA704610.1 GI:2714528 EST. human. Homo sapiens Eukaryota; Metazoa; Cho. Mammalia; Eutheria; Prii 1 (bases 1 to 467) Hiller,L., Allen,M., B Krizman,D., Kucaba,T., J., Moore,B., Schellen	2.2 987 12 CNSULOFF ALIGNMENTS	2.2 287 10 BF759346 2.2 319 10 BI028532 2.2 319 12 CNS0165X	2.2 2/5 10 BG01545 2.2 276 10 BG015456 5 5 5 70 10 BG978282	549 9 AA521406 583 9 AA521406 280 10 BG998167 1101 12 CNS0182P	2.3 205 10 B094703* 2.3 267 10 B0961378 2.3 1027 12 CNS0167 2.2 306 9 AA668797 2.2 316 10 B1004597 2.2 316 10 B1004597	2 2.5 506 10 BG659530 2 2.4 1101 12 CNS0039G 7 2.4 1101 12 BI029879 5 2.3 286 10 BI045052 6 2.3 343 10 BI045083 6 2.3 343 10 BI045083 4 2.3 169 10 BG998195	4.4 300 9 AU100132 4.1 932 9 AL542093 . 3.7 1052 10 BM455788 3.4 285 10 BM090262 3.0 899 9 AL540709 3.8 1101 12 CNS0039G
h LINL; contact the further information.  leen_INFLS_S1"  leen_INFLS_S1"  on fetus"  stant)"  stant)"  ector: pT7T3D (Pharmacia)	LS, MO 63108	l Homo sapiens cDNA l Homo sapiens cDNA ebrata; Euteleostomi; minidae; Homo. Geisel,G., Jost,S., n.G., Marra,M., Martin Tan,F., Theising,B., R.		BF/59346 KC2/CLOST BI028532 MR4-MT033 AL106335 Drosophil AL106663 Drosophil	BG978282 RC4-CI019 BG978282 RC4-CI019	AA521406 aa68c09.s BG998167 MR4-HT126 AL108811 Drosophil BI005814 MR4-HN005	BG961378 MR4-CT053 AL106813 Drosophil AA668797 aa80d11.s BI004597 MR4-HN005 AA521324 aa68e09.s	AL063921 Drosophil AL063921 Drosophil BI029879 IL0-MT035 BI045052 MR4-CT019 BI045083 MR4-CT010 BG998195 MR4-HT126 BG9991954 MR4-HT126	AU100132 AU100132 AL542093 AL542093 BM455788 AGENCOURT BM090262 505440 MA AL540709 AL540709 AL063921 Drosophil

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                    421 GAAGGGAGAGGTTGCAGAGTGAGGTGCAGAGCTTGGTGGACGATG 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TATTAGATGCTCAGAGTGTGTGCACAAGGCTGGCACGCCCCAGGGTCTTCCTCATGGCACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 tattagatgctcagagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcact 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 acatttttttatttaaatgaacttttcattttggaatagttttaggatttcaaaaattt 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACATTTTTTATTTAAATGAACTTTTCATTTTGGAATAGTTTTAGGATTTCAAAAAATTT 60
                                                                                                                                                                                                                                                                                                                                                                                                      ATGAACAGTGGGCTAAGCAAAGGGTTATTAATGTGTTATTAATGGGTTGAATCTAATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGCAGTGACAGATGCAAAACACAGGGTGATGGAAAGCCCTCAGGAGGGTAACCTAACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaacctaacc 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAGTCTACTGAAAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACTGGTGGTA 240
                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAGATAATACAGAGAATGCCCATATACCATCCTCCTTATCCCACTTCTTTTTGTGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                       603049567F1 NTH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                           BI763679.1 GI:15755257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466;
Sequencing by: Incyte Genomics, Inc.
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Pred. No. 7.3e-74;
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                                                                                                                                                                               2632 tctctttcttcttttgccctttcttagcttgc 2663
                                                                                                                                                                                                                                            2572 tototttaagactgtaagtogoctgoctgagtggtttoattttgtttttgtttttctgocot 2631
                                                                                                                                                                                                                                                                                                                     2513 ttaccgttt-tttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattc 2571
                                                                                                                                                                                                                                                                                                                                                                                          2453 cggcaccttttcttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgt 2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2333 gcgggggcggggagagagcctgcagccttcagaacagatattgctcattttctggcagtt 2392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 TTACCGTTTCTTTATTGTCACACAGAAAAAGAAACTGCCTTGTCTCCCCTTCCGGGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2213 aagctttagggtcgctggagggggaccccggttggagaggggagcggaactcctggacaa 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                               272 CTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAA 213
                                                                                                                                                                           32
                                                                                                                                                                                                                            92 TCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTTGTTTTTCTGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 AAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACTCCTGGACAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                             TCTCTTTCTTCTTTTGCCCTTTCTTAGCTTGC 1
                                                                                                                                                                                                                                                                                                                                                                        CGGCACCTTTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGGGGGGGGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTT
                                 2f55b04.sl Soares retina N2b4HR Homo sapiens cDNA clone MAGE:380815 3', mRNA sequence.
AA058563.1 GI:1551370
                                                                              AA058563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11474 row: e column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 colong the following pool of 2 oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full length clones and was constructed by C. 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:5189752"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host-"DH10B"
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Pred. No. 5e-69;
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2768 gttttgaaaagtccctcgctcagaaatgccagcttgcagatggctaatcaaagagacgtg 2827
                                                                                                    121 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Le, N., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moores, M., Parsons, J., Prange, C., Rifkin, L., Rohifing, T., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohifing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marza, M. Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marza, M. Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                   Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044478
                                                                                                                                                                                                                                                                                                         299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov) for Insert Length: 921 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Soares and M.Fatima Bonaldo.
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Local Similarity
                                                                                                                               Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DHIOS (amplicillin resistant)"
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/db_xref="GDB:1288949"
/db_xref="taxon:9606"
/clone="IMAGE:380692"
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/dev_stage="55 year old"
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                                                                                                                                                                                                                                                                                                        10.4%;
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                                                                                                                                                                                                                                                                                                        Score 294.4; DB 9; Length 577; Pred. No. 4.1e-43;
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 844 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
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The WashU-Merck EST Project
Unpublished (1995)
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.
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ZE344002.51 Soares retina N2b4HR Homo sapiens cDNA clone

IMAGE:360867 3', mRNA sequence.
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                                                                                            University of Toronto. Lacasida Soares and M.Fatima Bonaldo.
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/dev_stage="55 year old"
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/db_xref="GDB:1277412"
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      10.1%;
99.0%;
Score 286.4; DB 9
Pred. No. 1.1e-41;
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                 DB 9;
           Length 442;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aagtogotgoctgagtggtttcattttgttttgttttctgcocttctcttttcttcttt 2646
                                                                                                                                                                                                                                                   High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
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/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1
                                                                                                       /clone_lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:380300"
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:1288557"
                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                        Unpublished (1995)
Contact: Wilson RK
                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 339.
                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. | Louis, MO 63108
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/organism="Homo sapiens"
/db_xref="GDB:1289526"
                                                                            ocation/Qualifiers
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Pred. No. 1.1e-41;
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467 bp mRNA linear EST 30-JAN-1990 AA020992
ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Gish, W., Hawkins
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
Chissoe, S., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E.,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Rohlfing, T.,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
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/clone="IMAGE:381269"
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                                                                                            2768 gttttgaaaagtccctcgctcagaaatgccagcttgca 2805
                                                                                                                         2708 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 2767
                                                                                                                                                             2648 ccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctggggttggtgg 2707
                                                                                                                 182 TACTCGTTCCCACCGCACAGAACCCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT 241
                                                                                                                                                                                                 242 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCA 279
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              ys95e09.s1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222568 3', mRNA sequence.
                                              H84298
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                 /tissue_type="retina"
/dev_stage="55 year old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:363877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:1280580"
                                                                                                                                                                                                                                                                                  9.88;
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                                                                                                                                                                                                                                                           Score 276.4; DB y; Lung
Pred. No. 7.2e-40;
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                                                                                     2678 ttctgcttggtctcctgctggggttggtggtactcgttcccaccgcacagaacccggcgc 2737
                                                                                                                                                           2618 tgtttttctgcccttctctttttttttgccctttcttagcttgcactcccatggtgat 2677
                                                                                                                                                                                                           SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                          61 TGTTTTTCTGCCCTTCTTTTCTTTTTTGCCCCTTTCTTAGCTTGCACTCCCATGGTGAT 120
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                                                                                                                                                                                                                                                                                                                   Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: Promega -21m13
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1 (bases 1 to 376)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., R., Williamson, A., Wohldmann, P. and Wilson, R. Washu-Merck EST Project

The Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H84298.1 GI:1062969
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                                                                                                                                                                                                                                                                                                                                                                                               Soares and M.Fatima Bonaldo.
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/db_xref="GDB:3851329"
/db_xref="taxon:9606"
/clone="IMAGE:222568"
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                                                                                                                                                                                                                                                                                   9.6%; Score 270; DB 10; Length 3. 100.0%; Pred. No. 1e-38; Indels
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1 GTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTT 60
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1 (bases 1 to 398)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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Seq primer: Promega -21m13
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High quality sequence stops: 378
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo.
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a /note="Organ: eye; Vector: pT7T3D (Pharmacia) with a /notified polylinker; Site_1: Not|I; Site_2: Eco RI; 1st modified polylinker; Site_1: Not|I; Site_2: Eco RI; 1st modified polylinker; Site_1: Not|I; Site_2: Eco RI; 1st modified polylinker; 1st modified primer [5', pt]
strand cDNA was primed with a Not|I = Oligo(dT) primer [5', pt]
strand cDNA was primed with a Not|I = Oligo(dT) primer [5', pt]
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/db_xref="taxon:9606"
/clone="IMAGE:222494"
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The WashU-Merck EST Project
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                     59
    double-stranded cDNA was size selected, ligated to Eco RI double-stranded cDNA digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector the PTT3 vector old (pharmacia). The retinas were obtained from a 55 year old (pharmacia) and total cellular poly(A)+ RNA was extracted 6 Caucasian and total cellular poly(A)+ RNA was kindly hrs after their removal. The retina RNA was kindly hrs after their removal. The retina RNA was kindly hrs after thoronato. Library constructed by Bento University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="55 year old"
/dev_stage="55 year old"
/lab_host="0H10B (ampicillin resistant)"
/note="0rgan: eye; Vector: pT7T3D (Pharmacia) with a
/note="0rgan: eye; Vector: pT7T3D (Pharmacia) with a
/note="0rgan: eye; Vector: pT7T3D (Pharmacia) with a
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modified polylinker; Site_1: Not I: oligo(dT) primer
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/db_xref="GDB:1279093"
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 882 Std Error: 0.00 Seq primer: Promega -21m13 High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGAAAAGTCCCTCG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
High quality sequence stops: 361
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yt0461:s1 Soares retina N2b5HR Homo sapiens cDNA clone
IMAGE:223321 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H86544.1 GI:1068123
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                   /clone_lib="Soares retina N2b5HR"
                                                                                                                                                                                     /tissue_type="retina"
                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                             /clone="IMAGE:223321"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:3854355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 254.4; DB 9; Length 297; 99.6%; Pred. No. 6.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2618 tgtttttctgcccttctctttcttttgccctttcttagcttgcactcccatggtgat 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AGCTTGCAGATGGGCTAATCAAAGGAGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2558 ccttccgggaattctctctttaagactgtaagtcgctgcctgagtggtttcattttgttt 2617
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          High quality sequence stop: 269
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 419)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., R., Williamson, A., Wohldmann, P. and Wilson, R., Waterston The Washurdersk EST Project
                                                                                           High quality sequence stops: 269
                                                                                                          Email: est@watson.wustl.edu
Insert Size: 958
                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                          Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           v9302/
y922910.s1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:274746 3', mRNA sequence.
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Location/Qualifiers

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BASE COUNT
ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                             SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2810 gctaatcaaagagacgtg 2827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2750 aagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatg 2809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GCTAATCAAAGAGACGTG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGNTCAGAAATGCCAGCTTGCAGATG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197;
                                                                                                                                                                                                                                                                                                                                                                                     AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence.
AV715411
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                                                                                                                                                                                                                                                                                                                                                                  AV715411.1 GI:10796928
              Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
251 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                       xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vértebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               Unpublished (2000)
                                                                                                                                                    Homo sapiens cDNA DCB clones
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                             (bases 1 to 696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. " 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector the Not I and Eco RI sites of a modified pT7T3 vector.
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/clone="IMAGE:274746"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares retina N2b4HR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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99.5%;
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Pred. No. 1.4e-25;
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FEATURES
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                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             603083875F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222802 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI838027.1 GI:15949577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI838027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence
                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11560 row: f column: 19
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                   National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                         High quality sequence stop: 813.
                                                                                                                                                                                                                                                                                                                                                                                   (bases
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141 c 156 g 189 t
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/lab_host="BM25.8"
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/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo
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Search completed: September 7, 2002, 14:51:57 Job time: 16216 sec
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                                                                                   2586 taagtcgctgcctgagtggtttcattttgtttttgtttttcttgccc 2630
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## ALIGNMENTS

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                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2380)
1 (bases 1 to 2380)
Mueller-Schilling,M., Krammer,P. and Oren,M.
Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 3 03-FEB-2000;
Patent: DE 19847779-C 3 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
Location/Qualifiers
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Sequence 3 from Patent DE19847779.
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substances potentially useful for curve or patent: DE 19847779-C 4 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)		JOURNAL	
I (bases I to 2827)  1 (bases I to 2827)  Mueller-Schilling, M., Krammer, P. and Oren, M.  Mueller-Schilling, M., Krammer, P. and Oren, M.  Novel receptor dna useful for identifying apoptosi  Novel receptor dna useful for cancer chemother		FERENCE AUTHORS TITLE	RE
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                                                                                                                                                                   2341 cagaaatgccagcttgcagatggctaatcaaagagacgtg 2380
                                                                                                                                                                                                             2728 AACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAAGTCCCTCGCT 2787
                                                                                                                                                                                                                              2281 aacceggegeetattattggecaagaaacttgageageetgttttgaaaagteeeteget 2340
                                                                                                                                                                                                                                                                                                                                                            2161 cattttgtttttgtttttctgcccttctctttcttctttttgccctttcttagcttgcactc
                                                                                                                                                                                                                                                                                                                                                                                                         2368 AGATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGT 2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1921 agatattgctcattttctggcagttctcagacgtaggaaataagtcagcaccgaagcagt 1980
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                                                                                                                                                                                                                                                                                              ccatggtgatttctgcttggtctcctgctgggggttggtactcgttcccaccgcacag 2280
                                                                                                                                                                                                                                                                                                                                              CATTITIGITITGTTTTTCTGCCCTTCTCTTTCTTCTTTTGCCCCTTTCTTAGCTTGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTTATTGTCACACAGAAAAGGAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9tgacttggctggagcctcaggggcggggcactggcacggaacacccctgaggccagccc 1680
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        AL157394.15 GI:15384622
                               complete sequence. AL157394
                                                       Human DNA sequence from clone
                                                                             AL157394
                                  187313 bp DNA ...... Clone RP11-399019 on chromosome
                                                               PRI 22-AUG-2001
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Db 142476 GGCTATAATGATAAGTATTAAGTAAGGAAGATCCACATATGTGAGTTGCTGGCTTATAAT 142535
                                                                                                                                                                                              Db 142416 AGCTTTTTTGGCTACATTTTTTTTTTTTGTAAAGTAAGTTTAATAATCACTCATCTCACTG 142475
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                                                                                                                  61 ggctataatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataat 120
                                                                                                                                                                                                                            1 agcttttttggctacatttttttatttgtaaagtaagtttaataatcactcatctcactg 60
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate solves and the stranded or sequenced with an alternate solves are stranded or sequencing problems, such one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw:, currenament. The company of the consumer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304I5 is at 18704 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chr10
RP11-99019 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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/note="Sequence from AC015461 sequenced by WIBR."
105808. 1.05972
/note="Sequence from AC015461 sequenced by WIBR."
/note="Sequence confirmed by AC015461 sequenced by WIBR."
/note="sequence confirmed by AC015461 sequenced by WIBR."
a 36398 c 36888 g 58358 t
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/clone_lib="RPCI-11.2"
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/db_xref="taxon:9606"
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144876 ACCGTTTTTTATTGTCACACAGAAAAAGAAACTGCCTTGTCTCCCCTTCCGGGAATTCTCT 144935
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                                                                    99ctataatgataagtattaagtaaggaagatocacatatgtgagttgctggcttataat 120
                                                    GGCTATAATGATAAGTATTAAGTAAGGAAGATCCACATATGTGAGTTGCTGGCTTATAAT 567
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Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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784 c 809 g
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84.9%;
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               1201 gccaaggctcctgtacccaggcaggacctctgcgctctgagctccattctccttcaagac 1260
                                                                  1587 CAACATGGACAGCCAGTCAAATGCCCCGCAAGTCTTTCTCTGAGTGACTGCCAGCAATTA 1646
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 2344)
                                                                                                                                                                                                                                                                                                                                                                                          beta interferon; CD95 gene; silencer.
                                                                                                                                                                                                                                                                                                                                                                                                     x87625.1 GI:902311
                                                                                                                                                                                        Submitted (26-MAY-1995) F.H. Rudert, Genesis Research Development, Corporation Ltd., PO Box 50, Auckland, NE Overlaps with x81335, & x82279-X82286.
                                                                                                                                                                                                                                                                                                                    Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
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                                                                                       /map="q24
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                                                                                                   /tissue_type="placenta"
/map="q24.1"
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961 gaatgtttaatatagctggggctatgcgatttggcttaagttgttagctttgttttcctc 1020
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                                                                                                                                                                                                                                                                                                                                                                                           2065
                                                                                                                                                                                                                                                                                                                                                                                                                                               1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1825 CTCCCCAACTTCCCAGGTTGAACTACAGCAGAAGCCTTTAGAAAGGGCAGGAGGCCGGCT 1884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1261 ctccccaacttcccaggttgaactacagcagaagcctttagaaagggcaggaggaggccggct 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAAGAGTGACACAGAGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGA 2184
                                                                                                                                                                                                                                                                                                                                                                aggetteetteeeateeteetgaeeaeeggggettttegtgagetegtetetgatetege 1560
                                                                                                                                                                                                                                                                                                                                                      AGGCTTCCTTCCCATCCTGACCACCGGGGCTTTTCGTGAGCTCGTCTCTGATCTCGC
Direct Submission
           Nakanishi, y
                                factor for interleukin-6 expression upon in J. Biol. Chem. 270 (30), 18007-18012 (1995) 95355401
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2165)
                                                  Transcription stimulation of the Fas-encoding gene by nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGAGGTCCTCACCTGAAGTGAGCATGCCAGCACTGCAGGAACGCCCCGGGACAGGAA 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wada.N., Matsumura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                             Homo sapiens blood DNA, clone pF7.
                                                                                                                                            Fas antigen.
                                                                                                                                                     D31968
D31968.1 GI:961455
                                                                                                                                                                   Human DNA for Fas antigen, promoter region
                                                                                                                                                                                        HUMFAS
                    (bases 1 to 2165)
                                                                                                                                                                                  2165 bp
                                                                                                                                                                                 DNA
                                      influenza virus infection
                                                                                                                                                                           linear
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	_	Qy 421 ggcactaacagtctactgaaaggtggaacagagacaagcctatcaacaccaccaccaccaccaccaccaccaccacca
. <sub>+</sub>		
1442 CGCGCGC		Oy 361 tgtgtctattagatgctcagagtgtgtgcacaaggctggcacgcac
		_
1441	_	Qy 301 aaatttgcagagataatacagagagaatgcccatataccatcctcctcatctctctc
. µ		242
322		241 ctttttacatttttttatttaaatgaacttttcattttggaatagttttaggatttcaaa
Qy 1321 ctcgaggtcctcacctga		
Db 1262 CTCCCCAACTTCCCAGGT		181 cettecattecttecettacetecettecetteceteaeaeaeceetttteettee
Qy 1261 ctccccaacttcccaggt		122 TCACACTCAAGAGATACTGATTTTGTCAATTGTCCTTTTCCCCTTTTTTTT
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Qy 1201 gccaaggctcctgtaccc		Qy 61 99Ctateat9dcady.caccady.
Db 1142 CAACATGGACAGCCCAGTC		
1141		Qy 1 agctttttggctacactctctctacts
1082 TTTTTCATATGGTTAACT		Matches 1714; Conservantive Co
1081	0;	
1022 TTGAGAAATAAAAACTAA		70 04.
Qy 1021 ttgagaaataaaaactaag		
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Qy 961 gaatgtttaatatagctgg		
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901		CDS 1/82>101 /codon_start=1
		xon
841	<del></del>	14361781
Db 782 ATGTCATTATCCAAACATAC		12981306
781	уо	
722	מת	protein_bind 934940 Protein_bind mojety="AP-1"
y 721 aatactgaaacctttagtgt;	Qy	protein_bind 772780 /bound_moiety="NF-IL6"
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y 661 aattgggaagggagagaggtt	Qy	protein_bind 276284 /bound_moiety="NF-IL6"
602 TGAAGGA	Db	protein_bind 7987 /bound_moiety="NF-IL6"
601 tgaaggatgaacagtgggcta	QY	
542	Db	source /organism="Homo sapiens" /db_xref="taxon:9606"
541 ctaacctagatttgagggccc	ОУ	
482	ממ	Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.xauazama marrista mail:nakawa 920-0934, Japan (E-mail:nakanaka@dbs.p.xauazama marrista mail:n76-234-4424, Fax:076-234-4480)
481 gtggtaagtgcagtgacagats	Qy	JOURNAL Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Sournal Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa-11, 86, 10, 10, 10, 10, 10, 10, 10, 10, 10, 10
422 GGCACTAACAGTCTACTGAAAG	מם	

	п	ю	Qy Db	рb	Qy	DP DP	da Að	Db	Qy	Db Oy	Db	Qy	Qy Db	Db	Qy	Qу	Db	Qy	Qу	рb	Qy	Ωy	Db	Qy	Db 5	g B	
QY 1501 aggettectteceatectectgaccaccgggerial	GCGCGCAAGGTTUCTUAATCATTTUCTUATTUCTTTTTTTTTT	441 cgcgcgcaggccaagttgctgaatcaatggagccctccccaccca	1381 tgcccattg-ycac-ycac-ycac-ycac-ycac-ycac-ycac-yca	1322 CTCGAGGTCCTCACCTGAAGTWAWCAIGCCTCCCCCtgacttccccctgacttctcccccttccctac	1321 otogaggtcotcacotgaagtgagcatgocaggcactgoggagaacgccocgggacaggac   11321 otogaggtcotcacotgaagtgagcatgocaggcactgoggagaacgccocgggaCaggaA 138	1261 ctccccaacttcccaggttgaactacagcagaagcccccccc	1201 gccaaggctcctglaccccaggcygcygcygctlllllllllllllllllllllllllll	1142 CAACATGGACAGCCCAGTCAAATGCCCCGCAAVICIIIICCCCATTCTCCAGGACATGCACAATGAAATGCCCCGCAAVICIIIICCCAATGCAATGAAATGCCCAATGCAAAATGCAAAAATGCAAAAAAAA	1141 caacatggacagccagtcaaatgccccgcaagtctttctctgagtgactccagcaatca 200	1081 ttttcatatggtcaaccgcccarrictallilililililililililililililililililil	22 TTGAGAAATAAAAACTAAAAAACTAAAAAACAAAAAAAAA	agaaataaaaactaaggggccctcccttttcagggcccccacyyyy	ATTTGGCTTAAGTTGTTAGCTTTGTTTTCCT	TTTTTTTAAAGAAAATTGGCCAGGAAAAAAAAAAAAAAA	6		GTCATTATCCAAACATACCTTCTGTAAAA11CA1CCAGGGGGGGGGG	Caaacataccttctgtaaaattcatgctaaactacctaagggccaccaccaccaccaccaccaccaccaccaccacc	CCAAATTCAGGTTCAGTAAT	TTGGGAAGGGAGAGAGTTGCAAAATGAAAATGCAAATTCAAAAATTCAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAAA	anttgggaagggagaggttgcagagttgaggttgcagagcttggtggaggatgccaacy; anttgggaaggttg1		42 CTAACCTAGATTTGAGGGCCCCAAACAGGGGTtattaatgtgttattaatgggttgaatc	41 ctaacctagatttgagggcccaaacaggctccagaaggaaaatgtcaactggysgyscagaagaaaatgtcaactggysgyscagaacaggcaagcaactglillillillillillillillillillillillillil		tadtaaattacaattacaaattacaaaacacaaaattatataaattacaadcoctcaaaaadcoctcaadaadcaacaadaatacaataaacaadcoctcaadaadaaac	

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FEATURES
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Submitted (03-SEP-1994) P.H. Krammer, German Cancer Research
Center, Tumorimmunology Programm, Im Neuenheimer Feld 280, 69120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAGAGTGACACAGAGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCCGGTTTACGA 1621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krammer, P.
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1 (bases 1 to 1877)
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X81335
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                                                                                                Join(1670...1810, X81336.1:155...320, X81337.1:146...283, X81338.1:145...253, X81339.1:552...613, X81339.1:766...828, X81340.1:79...161, X81341.1:255...279, X81342.1:103...1757)
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1653. .1810
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                                                                                                                                                                                                                                            /usedin=X81335:HsmRNA1
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x81338.1:145. .253,x81339.1:552. .613,x81339.1:766. .828,
x81340.1:79. .161,x81341.1:255. .279,x81342.1:103. .1757)
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151. .261
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                                    .320, X81337.1:146. .283,
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301 aaatttgcagagataatacagagaatgcccatataccatccttcttatcccacttctttt 360
                                              COUNT
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                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APO-1 gene;
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                                                                                                                                                                                                                                                                                                                       Submitted (20-OCT-1994) J. Cheng, Univ.of Alabama at Birmir Univ. of Alabama, 701 South 19th Street, UAB Station, LHRB Birmingham, AL 35294-0007, USA Related sequences: M67454 and X63717.
                                                                                                                                                                                                                                                                                                                                                                                                           J. Immunol. 154 (3), 1239-1245 (1995) 95123075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                       gtgagcatgccagccactgcaggaacgccccggggacaggaatgcccatttgtgcaacgaa 1399
                                                                                                                                                                      GAACTACAGCAGAAGCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAA 1026
                                                                                                                                                                                    gaactacagcagaagcctttagaaagggcaggaggccggctctcgaggtcctcacctgaa 1339
                                                                                                                                                                                                                                                                                aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca 1219
                                                                                                                                                                                                                                                                                                                 TCCATTCCAGGAACGTCTGTGAGCCTCTCATGTTGCAGCCACAAGATGGACAGCCCAGTC
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                                                                                1362 ССАВАСЛАВСТССАВАВАВАВАТАТСАВСТВАВАВАВАВССТВАВАВАВТВАВСАВТВАВС
                                                                                                                                                                                           1422 АТАСААААСАСААААТААТААААААСССТСАААААААТААССТААССТАААТТТАААААС
740 tgtccagtctggaactgcatccaaattcaggttcagtaatgatgtcattatccaaacata 799
                                                                                                                                                                                                                                               1542 AAATATATACACAAAACTAACACGCCCAAAATCTTCCTCATAACACTAACAATCTACTAA 1483
                                                                                                                                                                                                                                                                                                                                                         1602 ACAAAAATACCCTATACCATCCTCCTTATCCCACTTCTTTTATATCTATTAAATACTCA 1543
                                         680 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 739
                                                                                             620 taagcaaagggttattaatgtgttattaatgggttgaatctaattgggaagggaggagg 679
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                                                                                                                                                      ccaaacaggctccagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggc 619
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Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with the immune
Patent: WO 0200928-A 2392 03-JAN-2002;
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Sequence 2391 from Patent W00200928
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 2 03-FEB-2000;
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                                                                                                                           DEUTSCHES KREBSFORSCH (DE)
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Mammalia; I
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                                                      /db_xref="taxon:9606"
181 c 216 q
                                                                            /organism="Homo sapiens"
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Score 611.8;

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6;

Length 720;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 TTACCGTTTTTTATTGTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 GCCCTGACAAGCCAAAGGTCCGCTCCGGCGGGGTGGGTGAGTGCGCGCCGCCCC
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: GTCTCCCTTCCGGGAATTCT
Primer B: AACCCCAGCAGGAGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t9Ct9999tt9gt9gtactcyttcccaccgcacagaacccggcgcctattattggccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttaccgttttttattgtcacacagaaaaggaaactgccttgtctcccttccggggaattct 2125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGGGGGGGGAGAGAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTT 285
                                                                                                                                      Contact: Michael Olivier, David R. Cox
                                                                                                                                                                                    1 (bases 1 to 398)
Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               909999909999agagagcotgcagcottcagaacagatattgctcattttcctggcagtt 1945
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                   62/038
SHGC-30908 Human Homo sapiens STS genomic, sequence tagged site.
G27038
                                                                                                                                                                                                                                                                                                                                 G27038.1 GI:1375288
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                                                                                       CA 94025, USA
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                                                                                               BC012479
                                                                                                          RESULT
          SOURCE
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ORGANISM
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                                                                                                                                        121 GTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAGAACCC 180
                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                270; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prepared with primer pairs provided by Sandoz, derived from H86126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buffer:
                                                              Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 6, clone MGC:21432 IMAGE:4514272, mRNA
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                     BC012479
 Homo sapiens
                                            BC012479
             numan
                                 BC012479.1 GI:15214691
                                                       complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University/Merck EST sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tag Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR Cycles:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tris-HCl:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Human"
                                                                                                                                                                                                                                                                                                                                                                            10.9%; Score 259; DB 11; 99.6%; Pred. No. 4.7e-56;
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62 degrees C:
72 degrees C:
30
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C for 23 seconds
C for 30 seconds
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                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                            PRI 20-AUG-2001
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1651 ctggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctcttctcc 1710
                                                                                                                                                                                                   1531 ggcttttcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacg 1590
                                                                                                                                                                      61 GGCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                    245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Series: IRAK Plate: 28 Row: i Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 2719)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily, member 6"
/protein_id="AAH12479.1"
/db_xref="GI:15214692"
/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
ETQNLEGIHHDGQFCHKPCPPCERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCRLCDEGHGLEVEINCTRTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIIKECTLT
SNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPE
TVAINLSDVDLSKYITTIAGVWTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref=-taxon:9606"
/db_xref=-taxon:9606"
/clone="MGC:21432 IMAGE:4514272"
/clone=type="Bladder, transitional cell papilloma"
/clone_lib="NIH_MGC_93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Similar to tumor necrosis factor receptor
superfamily, member 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 245; DB 9; Length 2719; 100.0%; Pred. No. 2.6e-52; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1318
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ORIGIN
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       y Match
9.1%; Score 216; DB 9; Length 702;
Local Similarity 100.0%; Pred. No. 7e-45;
hes 216; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 702)

Muschen, M., Re, D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R. and Rajewsky, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muschen, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 702)
Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo-1 Fas; CD95 antigen; CD95 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences: D31968 X89101 AJ279012 AJ279013
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        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CGCAAGAGTGACACACAGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGGAAGCGGTTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacg 1619
                                                                                                                                                                                                                                                                                                                                                                                               Related sequences: D31968 X89101 AJ279011 AJ279013
                                                                                                                                                                                                                                                                                                                                                                                                                           Koeln,
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 702)
Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muschen,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 side-effect of the germinal center reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Somatic mutations of the CD95 gene in human B cells as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 702) Muschen, M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuppers, R.
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Apo-1 Fas; CD95 antigen; CD95 gene.
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                                                                                                                                                                                                                                                                     ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                       pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                           1372.8
879.4
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                                                                                                                                                                                                                                                                        Score
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Listing first 45 summaries
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                                                             AAQ93879
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                                   Human colon cancer
Human CD95 recepto
DNA encoding a hum
Fas-delta-TM CDNA.
Soluble Fas recept
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Human immune syste
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           Human cell surface
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RESULT AAT34162 standard; DNA; 1608 BP Fas gene promoter; apoptosis; ageing; autoimmune disease;  $\mathtt{T}\text{-cell}$  senescence; ss. AAT34162; Fas promoter region. 22-OCT-1996 ٢ (first entry)

ALIGNMENTS

AAT34162
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XX
AC AAT3
AC AAT3
XX
PAS
XX
FAS
XX
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protein\_bind

168..174

protein\_bind

protein\_bind

/\*tag= e

/\*tag= d /function= Myb transcription factor binding site /note= "claim 9" 349..353

/function= EBP20 transcription factor binding site 272...276

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Matches 1388;
                                                                                                                Query Match
Best Local
                                                                                                                                                                                              defined as the Fas gene promoter region. This includes a number of transcription factor binding sites. A coding sequence for the N-terminal portion (AAR99471) of the Fas protein leader peptide is also included. The DNA segment was isolated from a human ras cDNA placental DNA library using a 32P-labeled segment of human ras cDNA corresponding to nt 23-346. It can be combined with a structural gene so that the gene is under the transcriptional control of the transcription factor binding sites. The promoter region can be used to regulate Fas gene expression, e.g. in tumour or immune cells, as a means of treating Fas-mediated apoptosis disorders such as
                                                                                                                                                          Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;
380 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 439
                                            320 agagaatgcccattataccatcctccttatcccacttctttttgtgtctattagatgctca 379
                                                                                                                                                                                            malignancies and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                          Claim 11; F1g 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                        A novel
                                                                                                                                                                                                                                                                                                                                                                                                             Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas-mediated
                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis disorders
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Local_Similarity 99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koopman WJ,
                                                                                              Conservative
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/product= Fas protein leader
1497..1608
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1075..1476
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/note= "claim 8"
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                                             ccctgactccttcctcaccctgacttctccccctccctacccgcgcgcaggccaagttgc 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 2392.
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                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, heurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/vlacerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-130909/17.
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   Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 other;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 agagaatgcccatataccatcctccttatcccacttctttttgtgtctattagatgctca 379
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                                                                                                                                                  1160 aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca 1219
                                                                                                                                                                                             1340 gtgagcatgccagccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaa 1399
                                                1280 gaactacagcagaagcctttagaaagggcaggaggccggctctcgaggtcctcacctgaa 1339
                                                                                                                                                                                                                              882 AAACCCTCCCTTTTCAAAACCCCTATAACGCAACATCTATACTTTTTCATATAATTAACTA 823
                                                                           ATACAAAACACAAAATAATAAAAAACCCTCAAAAAAATAACCTAACCTAAATTTAAAAAC 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atgcaaaacacagggtgatggaaagccctcaggagggtaacctaacctagattttgagggc 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ССАРАСЛАДСТССАРАВЛАВАВАНТАТСРАСТВРАВЛАВАВЛЕСТВРАВЛАВТАВАСТВРАВС 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccaaacaggctccagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggc 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACAAAATAAAATACAAAACTTAATAAACGATACCAAAAAAATACTAAAACCTTTAATA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgtccagtctggaactgcatccaaattcaggttcagtaatgatgtcattatccaaacata 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg
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                                                                                                                                                                                                                                            gggcctoccttttcagagccctatggcgcaacatctgtactttttcatatggttaactg 1099
                                                                                                                                                                                                                                                                                                      ggctatgcgatttggcttaagttgttagctttgttttcctcttgagaaataaaaactaag 1039
                                                                                                                                                                                                                                                                                                                                AACCAAAAAATAATAAATAACGAAAAACAAAAAATAATTATAAATATTTAATATAACTAA 943
                                                                                                                                                                                                                                                                                                                                               ggccaggaaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg
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77.1%;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                 Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 2391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL34418 standard; DNA; 1608 BP
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Best Local :
                 1172 agtotttototgagtgaotocagcaattagocaaggotoctgtacocaggoaggaootot 1231
                                                                                                                                                           1052 ttcagagccctatggcgcaacatctgtactttttcatatggttaactgtccattccagga 1111
859 agtttttttttgagtgattttagtaattagttaaggtttttgtatttaggtaggattttt
                                                                                                                                                                                                                                                                                  619 atgagtaacgaaggataggaagtaattgtgaatgtttaatatagttggggttatgcgatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                             812 ttcatgctaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo: leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 tagaagaaaatgttaattgagaggaagtttgaaggatgaatagtgggttaagtaaagggt 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 cagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggctaagcaaagggt 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 aaggotggoacgoccagggtottootoatggcactaacagtotactgaaaggtggaacag 451
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                                                                                        acytotytyaycototoatyttycaycoacaacatyyacaycocaytoaaatycocogca 1171
                                                                                                                                        tttagagttttatggcgtaatatttgtatttttttatatggttaattgtttattttagga 798
                                                                                                                                                                                                                               tggottaagftgfttagctttgttttcotottgagaaataaaaactaaggggccctccctt 1051
                                                                                                                                                                                                                                                                                                     atgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctggggctatgcgatt 991
                                                                                                                                                                                                            gtttattagagtacgaaagaattataagatttttttttaaagaaattggttaggaaata
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76.7%;
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Pred. No. 5.7e-229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            979 aagtttttagaaagggtaggaggtcggttttcgaggtttttatttgaagtgag-atgtta 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; reproductive disorder; gastrointestinal disorder; renal disorder; medications disorder; renal disorder; respectives disorder; renal disorder; respectives disorder; renal 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC98177 standard; cDNA; 859 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1712 gcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
12-MAR-1999;
                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious disease;
                                                            P-PSDB; AAB53420
                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                              Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcttttcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacgc 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gttattgtaggaacgtttcgggataggaatgtttatttgtgtgtaacgaattttgatttttt 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtttttcgtgagttcgtttttgatttcgcgtaagagtgatatata¦ggtgtttaaagacgt 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcgg 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggcacggaacacaccctgaggccagccctggctgcccaggcggaggtgcctcttctccc 1711
                                                                                        2000-587534/55.
                                                                                                                                                                                                                                                              99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disorder; ss.
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밁
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ88700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, proteins and antibodies to the proteins are useful for the prevention, proteins and allowed to the proteins are useful for the prevention, polynucleotides may be used in disgnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune may also be used to prevent diseases such as neural disorders, system disorders, muscular disorders, reproductive disorders and disorders, and cardiovascular disorders. AAC98764 to AAC98772 and diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98707 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1508 cttcccatcctcctgaccaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1568 tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ88700 standard; DNA; 266 BP.
                                                                                                                                                                          protein_bind
                                                                                                                                                                                                                                                                 cancer chemotherapy; ss.
                                                                                                                                                                                                                                                                                p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                                                    Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                                                      11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                            AAZ88700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 ccaggcggagctgcctcttctcccgcgg 226
 16-OCT-1998;
                                                                    03-FEB-2000
                                                                                                        DE19847779-C1.
                                                                                                                                                                                                                               Homo sapiens
                                   16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 cgtccgcccacgcgtccgaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ψı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccaggcggagctgcctcttctcccgcgg 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctggagcctcaggggcgggcactggcacggaacacccctgaggccagccctggctgc 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
 98DE-1047779
                                     98DE-1047779
                                                                                                                                                                               160..179
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                           /bound_moiety= p53
                                                                                                                                                              *tag= a
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94.7%;
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0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
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WPI; 2000-628395/60
                                                                                                                                                                            12-APR-1999;
                                                                                                                                                                                                                          10-APR-2000; 2000WO-US09540
                                                                                                                                                                                                                                                                                                                                                   WO200061150-A1.
                                                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                            19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis; Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC61798 standard; DNA; 2551 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1886 gcgggggcggggagagagcctgcagccttcagaacagatat 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1766 aagctttagggtcgctggagggggaccccggttggagaggaggggggaactcctggacaa 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 gcggggggggggagaggcctgcagccttcagaacagatat 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 aagotttagggtogctggagggggaccccggttggagagaggagcggaactcctggacaa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-162245/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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                                                      Marcusson EG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                   9905-0290640
                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 161; DB 21; 100.0%; Pred. No. 9.3e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 266;
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    Barr PJ,
                          (LXRB-) LXR BIOTECHNOLOGY INC.
                                                      15-NOV-1993;
                                                                                15-NOV-1994;
                                                                                                          26-MAY-1995
                                                                                                                                   W09513701-A
                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
adoptive immunotherapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                              Fas-delta-TM cDNA.
                                                                                                                                                                                                                                                                                                                                                    06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     AAQ93879 standard; cDNA; 2471 BP.
                                                                                                                                                                                                                                                                                                                                                                                   AAQ93879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1621 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1561 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacga 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslated or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas plusphatase). The antisense compounds are used to inhibit the expression of Fas, FasL or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They are not also be used to treat cancer, especially colon, liver or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 tggctgcccaggcggagctgcctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 71-73; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (Fap-1) expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB19341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 gtgacttggctggagcctcaggggcggggcactggcacggaacacaccctgaggccagccc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%; Pues 155; Conservative 0;
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  Kiefer MC,
                                                     93US-0152443.
                                                                              94WO-US13173
                                                                                                                                                                     /*tag= b
243..1136
                                                                                                                                                                                             /*tag= a
195..242
                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                   Location/Qualifiers
Shapiro JP;
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100.0%; Pred. No. 1.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli pH5-alpha cells. insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR76238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-200120/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig.3-1 to 3-4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1707 ctcccgcgg 1715
                                                                                                                                                                                                                                                                                                     Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                                       Soluble Fas receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX24878 standard; DNA; 2471 BP.
                                                                                                                                                                                                                                                                     Mammalia.
                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 5.4%; Score 129; DB 16;
Local Similarity 100.0%; Pred. No. 3.2e-25;
hes 129; Conservative 0; Mismatches 0;
                        16-JUL-1998;
                                                                             W09903999-A1
                                                                                                              polyA_signal
                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
    17-JUL-1997;
                                                    28-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
  97US-0052829
                            98WO-US14771.
                                                                                                                                                                  /*tag= b
243..1136
                                                                                                                /*tag= d
2455..2460
                                                                                                                                                                                          /transl_except= (pos:519..521, aa:Gly)
195..242
                                                                                                                                           /*tag= c
2349..2354
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                  В
AAQ29959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (Fasl). In some embodiments, Fasl is coadministered of Fas ligand (Fasl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-132243/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW98070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1587 gacgcttctggggggtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     1707 ctcccgcgg 1715
                                                                                                                                                                                                                                                                                        AAQ29959 standard; cDNA to mRNA; 2534 BP
               mat_peptide
                                                sig_peptide
                                                                                                          Homo sapiens
                                                                                                                                         Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.
                                                                                                                                                                                  Human cell surface antigen.
                                                                                                                                                                                                                       12-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg
                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
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                                                                                                                                                                                                                                                                                                                                                                                    ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive agent, and the cell mixture comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                     /*tag= a
243..1199
                                                        Location/Qualifiers 195..242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.4%; Score 129; DB 20;
100.0%; Pred. No. 3.2e-25;
1ve 0; Mismatches 0;
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                   19-FEB-1996 (first entry)
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                                            AAQ95297;
                                                           AAQ95297 standard; cDNA; 2534 BP
                                                                                                                                                                                                                                                                                                           A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BstXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-Ab. The cells were then suspended in buffer containing murine anti-Fas antibodies. The Fas-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered cells and used to positive clone (pF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORF corresp. (i.e. human Fas antigen)
                                                                                                                                                                               1647
                                                                                                                                                                                                 1587 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                   121
                                                                                                                                                                                                                                                                                  Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 1 and 2; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR28084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-358914/44.
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                                                                                                                                                         99cact99cac9gaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                 ctcccgcgg 129
                                                                                                                                                                                                                                        129;
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2352..2357
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1831..1836
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1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                          5.4%; Score 129; DB 13; 100.0%; Pred. No. 3.3e-25;
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                                                                                                                        AAT16303
                                                                                                                                  RESULT 11
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Synthetic.
                                                                   06-SEP-1996 (first entry)
                                                                                          AAT16303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP07115988-A.
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                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                       129;
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                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                    Conservative
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195..242
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243..1199
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Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
                                                                                            hFas coding sequence from plasmid pCEV4/hFas.
                                                                                                                                                                                                                                                                          AAT16303 standard; cDNA; 2534 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1647 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1587 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody production; diseases; treatment; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pF58; human Fas cDNA; soluble membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pF58 contg. human Fas cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 195..1202
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100.0%; Pred. No. 3.3e-25;
tive 0; Mismatches 0;
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EX PX AX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9601277-A1.
                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the coding sequence for the human Fas antigen contained within the plasmid pCEV4/hFas. The soluble Fas antigen is included in the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas antigen encoded monoclonal antibody, as well as the standard soluble Fas antigen encoded by this sequence. The assay is simple and has high accuracy, high by this sequence of assaying a number of different specimens sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD. (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hachiya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 49-52; 124pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR92528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systemic lupus erythematosus
                                                                                          32993
                                                                                                                                                                                          Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;
                                                                                                                                                                        1707
                                                                          AAV32993 standard; cDNA; 2534 BP.
 Fas cDNA
                          18-NOV-1998
                                                  AAV32993;
                                                                                                                                          121 ctcccgcgg 129
                                                                                                                                                                                                                                               1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1996-087635/09.
                                                                                                                                                                                                                                                           ctcccgcgg 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95JP-0025637.
94JP-0154706.
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243..1998
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195..242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                             (first entry)
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Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL; CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV; simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylactic; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                      WO9835692-A1
                                                                                                                                                                                                                                                 Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                 17-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-1998.
                                                                                                                                                                                                                                                                                              WPI; 1998-456867/39.
                                                                                                                                                                                                                                                                                                                Screaton GR,
                                                                                                                                                                                                                                Disclosure; Fig 10; 71pp; English.
                                                                                                                                                                                                                                                                                    P-PSDB; AAW49104.
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                                                                                                                                                                                                                                                                                                                                                    97GB-0003276
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195..242
/*tag= b
243..1199
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1831..1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Fas protein"
```

The present sequence represents a Fas cDNA sequence used in the CC method of the invention. The method is concerned with reducing CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK) CC cells in an immune cell population which also comprises of Fas-ligand CC (Fasi)-expressing activated CD4+ cells. It involves contacting this CC (Fasi)-expressing activated CD4+ cells. It involves contacting this CC (Fasi)-expressing activated CD4+ cells. It involves contacting this CC (Fasi)-expressing contaction with an effective amount of an agent (e.g. a CC interaction between Fas and Fasi. Therefore, the method is useful for CC interaction between Fas and Fasi. Therefore, the method is useful for CC interaction to the agent in the manufacture of the apentic compositions. CC res-expressing CD8+ TK cells in immune cell populations. Also claimed CC is the use of the agent in the manufacture of therapeutic compositions. CC cell surface receptor Fas and its ligand Fasi. By interfering with CC cell surface receptor Fas and its ligand Fasi. By interfering with CC cell surface receptor Fas and its ligand Fasi. By interfering with CC apoptosis of CD8+ TK lymphocytes caused by expression of Fasi on CC apoptosis of CD8+ TK lymphocytes caused by expression of Fasi are activated CD4+ cells. Such Fasi-expressing activated CD4+ cells are extivated CD4+ cells. Such Fasi-expressing activated CD4+ cells are virus e.g. human immunodeficiency virus (HTV) or simian immunodeficiency virus e.g. human immunodeficiency virus (HTV) or simian immunodeficiency virus e.g. human immunodeficiency virus (HTV) activity continued to composition of apoptosis may then allow continued to composition of apoptosis and the cD4+ cells infection with the infectious agent, enabling continued to composition of activate continued to composition continued to composition of continued to continued to continue diseases e.g. AIDS.

Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

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δõ
                           Matches 129;
                                   Query Match
Best Local :
Local Similarity
                            Conservative
                                      100.0%;
                                      5.4%; Score 129; DB 19;
100.0%; Pred. No. 3.3e-25;
                               0;
                                Mismatches
                                                  DB 19; Length 2534;
                                    Indels
                                     0;
                                      Gaps
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The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted).

The derivatives are effective regulators of apoptosis and can be of the coding DNA in gene therapy) to treat a range of diseases, such as hepatits, influenza and HIV, by modulating apoptosis of virus-infected calls
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Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                                                         Disclosure; Fig 1-2; 102pp; Japanese.
                                                                                                                                                                           has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases
                                                                                                                                                                                                Fas antigen derivative containing modified extracellular region -
                                                                                                                                                                                                                                 P-PSDB; AAW50289
                                                                                                                                                                                                                                          WPI; 1997-558981/51.
                                                                                                                                                                                                                                                                Nagata S, Nakamura N;
                                                                                                                                                                                                                                                                                                                       02-MAY-1996;
                                                                                                                                                                                                                                                                                   (MOCH ) MOCHIDA PHARM CO LTD.
(OSAB-) OSAKA BIOSCIENCE INST
                                                                                                                                                                                                                                                                                                                                            01-мау-1997;
                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                       W09742319-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Fas antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV07002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV07002 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1707 ctcccgcgg 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                   96JP-0135760.
                                                                                                                                                                                                                                                                                                                                         97WO-JP01502.
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195..2
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                                                                                                                                                                                                                                                                                                                                                                                                     /product= Fas_antigen
                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                cis elements needed for replication and virion encapsidation but is deleted of all viral genes. It carries a mouse dystrophin virus that supplies the sequences needed for a productive viral adenovirus is produced that is characterized by high titer transgene transgene into the host cell chromosome. Such a vector can be used to transfer the dystrophin gene for use in muscular dystrophy gene
Sequence 19307 BP; 4816 A; 4393 C; 4056 G; 6042 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.4%;
Best Local Similarity 99.2%;
Matches 128; Conservative
                                                                                                                                                            Shuttle vector padDel.CMVDys (AAT27558) comprises the adenovirus
                                                                                                                                                                                              Example 9; Fig 12A-12P; 149pp; English.
                                                                                                                                                                                                                             transgene(s) to target cells
                                                                                                                                                                                                                              Recombinant adenovirus produced from shuttle vector and helper virus has crippled packaging function, useful for delivering
                                                                                                                                                                                                                                                                                                        Chen S, Fisher KJ, Weitzman M, Wilson JM;
                                                                                                                                                                                                                                                                                     WPI; 1996-251463/25.
                                                                                                                                                                                                                                                                                                                                         (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; dystrophin; muscular dystrophy; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9613597-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuttle vector pAdDel.CMVDys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT27558 standard; cDNA; 19307 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1647 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1587 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1707 ctcccgcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gacgcttctggggagtcagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                   94US-0331381
                                                                                                                                                                                                                                                                                                                                                                                            95WO-US14017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 127.4; DB 18;
Pred. No. 9.2e-25;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2534;
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Qγ

1667 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 1726

Matches Query Match Best Local :

93;

Conservative

0; Mismatches

49;

Indels

0; Gaps

Score 63.6; DB 17; Length 19307; Pred. No. 2.2e-06;

Local Similarity

2.7%;

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16048 ccggccgcctgcagctggcgccatcgatacgcgtacgtcgcgaccgcggacatgtacaga 16107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16168 tttacaacgtcgtgactgggaa 16189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1787 gggaccccggttggagagagga 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT27557 standard; cDNA; 9972 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; cystic fibrosis transmembrane conductance regulator; CFTR; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT27557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shuttle vector pAdDel.CBCFTRZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                          Sg
                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_unit
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                                                                                              09-MAY-1996.
                                                                                                                  WO9613597-A2
WPI; 1996-251463/25
                   Chen S,
                                                          28-OCT-1994;
                                                                             27-OCT-1995;
                                     (UYPE-) UNIV PENNSYLVANIA.
                   Fisher KJ, Weitzman M,
                                                          94US-0331381.
                                                                             95WO-US14017.
                                                                                                                                                                                                                                                                                                                                                                                          /note= "3' adenovirus inverted terminal repeat"
complement (3887..3684)
                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3652..3073)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                               /function= packaging sequence PAC I complement (9353..9340)
                                                                                                                                                                                                                                                                          /note= "5' adenovirus inverted terminal repeat" (complement (9374..9360)
                                                                                                                                                                                                                                                                                                                                                                          complement (8622..4065)
                                                                                                                                                                                                                                                                                     /rpt_type= INVERTED
/note= "5' adenoviron
                                                                                                                                                                                                                                                                                                                                               /function= CFTR gene
complement (9241..8684)
                                                                                                                                                                                                                 /function= packaging sequence PAC complement (9311. 9298)
                                                                                                                                                        /function= packaging sequence PAC IV complement (9276..9263)
                                                                                                                                                                                    /function= packaging sequence PAC III complement (9301..9288)
                                                                                                                                     /function= packaging sequence PAC V
                                                                                                                                                                                                                                                                                                                                                                                                                 INVERTED
                                                                                                                                                                                                                                                                                                                  CMV enhancer/beta actin promoter (9611..9254)
                      Wilson JM;
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B
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                 Best Local Similarity Matches 92; Conserv
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Shuttle vector pAdDel.CBCFTR (AAT27557 comprises the adenovirus cis elements needed for replication and virion encapsidation but is deleted of all viral genes. It carries a CFTR gene under the control of a chimeric CMV enhancer/Chicken beta-actin promoter. It is used with a helper virus that supplies the sequences needed for a productive viral infection but which has disabled packaging function. A productive viral infection but which has disabled packaging function a productive viral is produced that is characterized by high titer transgene delivery to host cells and the ability to stably integrate the transgene into the host cell chromosome. Such a vector can be used to transfer the CFTR gene for use in cystic fibrosis gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant adenovirus produced from shuttle vector and helper virus - has crippled packaging function, useful for delivering transgene(s) to target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 7A-7H; 149pp; English.
                                                                                                                                                                                                   1668 ctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
                                                                                                                                                                                                                                                                                                                                                                               Sequence 9972 BP; 2581 A; 2362 C; 2245 G; 2784 T; 0 other;
                                                                                     2920 CTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                                1728 ctcgagaagtactagtgggccagtggggcgtgcaccttaagctttagggtcgctggaggg 1787
                                                                                                                                                                           2980 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 2921
2860 TTACAACGTCGTGACTGGGAA 2840
                                        1788 ggaccccggttggagagagga 1808
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                              2.6%;
                                                                                                                                                                                                                                                                           0; Mismatches 49;
                                                                                                                                                                                                                                                                                                Score 62.6; DB 17; Length 9972; pred. No. 2.9e-06;
                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                         Gaps
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search completed: September 7, 2002, 18:41:53
Job time: 30007 sec

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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                               Result
                                             00000
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                                                                                                                                                                                                                                                                                                       Score
                                Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/

2: /cgn2_6/ptodata/2/

3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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Match Length DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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                       4476
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US-09-180-100-16
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US-08-232-463-14
US-08-836-022A-10
US-08-836-022A-3
US-08-836-022A-3
US-09-427-048A-3
US-09-427-048A-3
US-09-427-048A-3
US-09-427-048A-3
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US-09-427-048A-3
US-09-427-048A-3
US-09-018-584A-25

US-08-332-766A-8

US-08-632-906A-18

US-09-417-455-7

US-09-418-584A-9

US-09-018-584A-9

US-08-713-557B-35

US-08-480-784-26

US-08-480-784-24

US-08-483-553-24

US-08-487-002-24
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28 48 2.0 421 1 US-08-483-554B-24 29 48 2.0 421 4 US-08-488-011B-24 30 48 2.0 421 5 PCT-US95-10202-24 31 48 2.0 421 5 PCT-US95-10203-24 32 48 2.0 421 5 PCT-US95-10203-24 33 47.6 2.0 287 2 US-08-365-486A-11 35 47.4 2.0 1679 2 US-08-365-486A-11 36 47.4 2.0 1679 2 US-08-880-342-11 36 47.4 2.0 12141 4 US-09-488-671-10 C 37 47.4 2.0 80246 4 US-09-078-294-4 38 47.4 2.0 80595 4 US-09-078-294-3 39 47.4 2.0 80595 4 US-09-078-294-3 39 47.4 2.0 80595 4 US-09-108-584A-8 C 41 47.2 2.0 325 2 US-08-332-766A-11 C 41 47.2 2.0 325 2 US-08-332-766A-11 43 46.8 2.0 444 2 US-09-018-584A-19 45 45.6 1.9 388 2 US-08-623-906A-13 ALIGNMENTS  ALIGNMENTS	RESULT	000 0 0
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21222		421 421 421 421 421 421 627 1679 11679 12141 80246 80246 80246 446 446 446 446
US-08-483-554B-24 US-08-488-011B-24 US-08-850-727-24 PCT-US95-10202-24 PCT-US95-10202-24 PCT-US95-10202-24 US-08-332-766A-27 US-08-332-766A-11 US-08-880-342-11 US-08-880-342-11 US-09-488-671-10 US-09-488-671-10 US-09-078-294-4 US-09-078-294-3 US-09-078-294-3 US-09-018-584A-8 US-08-332-766A-11 US-08-332-766A-10 US-08-332-766A-26 US-08-332-766A-10 US-09-018-584A-19 US-09-018-584A-19 US-08-623-906A-13		114D550004444400040
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DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1
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                                                                                                              QΥ
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LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09290640 Patent No. 6204055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
                                                                                                                                                                                                                            Query Match 6.5%; Score 155; DB 4; Length 2551; Best Local Similarity 100.0%; Pred. No. 1.5e-32; Matches 155; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE: 15
PAGES: 10709-10715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      DATE: 1992-05-25
                                                                                                                                                                       1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
                                                                                             1621 gtgacttggctggagcctcaggggcgggcactggcacgggaacacaccctgaggccagccc 1680
    121
                                                                           61 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 120
                                                                                                                                                    1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
tggctgcccaggcggagctgcctcttctcccgcgg 155
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US-08-444-231-18

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US-08-152-443A-18
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                Sequence 18, Application US/08152443A Patent No. 5663070
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                      1707 ctcccgcgg 1715
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                                                                                                                    121 CTCCCGCGG 129
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LOCATION: 195.
FEATURE:
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REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        61 GGCACTGGCACGGAACACACCCTGAGGCCAGGCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
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FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICANT:
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LOCATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0:
FILING DATE: 18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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BHAPIRO, JOHN P.
KIEFER, MICHAEL C.
NVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
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; Sequence 1, Application US/08219237B
; Patent No. 5874546
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   GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: 1TOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 129;
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                  1647 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
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                                                                                                                                                                                                                .121 CTCCCGCGG 129
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
CLASSIFICATION:
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TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
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NAME: LEHNHARDT, SUSAN K
                                                                                                                                                                                                                                                                 61 GGCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
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APPLICANT:
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TELEFAX: 706141
Tex: 706141
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                1 GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide LOCATION: 243
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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STATE: California
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195..1136
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SHAPIRO, JOHN P.
KIEFER, MICHAEL C.
NVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                      5.4%; Score 129; DB 1;
100.0%; Pred. No. 1.9e-25;
ative 0; Mismatches 0;
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NAME: James W. Hellwege REGISTRATION NUMBER: 28,808 REFERENCE/DOCKET NUMBER: 5167 INFORMATION FOR SEQ LID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2534 base pairs
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                                           Matches
                                                                            Query Match
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
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LIBRARY: pCEV4
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1587 gacgottotggggagtgagggaagcggtttacgagtgacttgg\dot{
m p}tggagcotcaggggcg 1646
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                             FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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LOCATION: 195..1202
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                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat_peptide LOCATION: 243..1199
                                                                                                                                                    NAME/KEY: polyA_site LOCATION: 2518..2523 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                              NAME/KEY: polyA_site LOCATION: 2352..2357 IDENTIFICATION METHOD:
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                                         Local Similarity
les 129; Conserv
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                                       5.4%; Score 129; DB 2; Length 2534 ilarity 100.0%; Pred. No. 2e-25; Conservative 0; Mismatches 0; Indels
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1831..1836
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                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-205-800
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1647 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE TITLE OF INVENTION: ANTIGEN NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MURPHY JK., 28,977
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                             FEATURE:
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                                                       FEATURE:
NAME/KEY:
                                                                                                                FEATURE:
                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                    LENGTH: 2534 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                         LOCATION:
                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                            ORGANISM:
                                                                                    LOCATION:
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                                                                                                                                                                         sig_peptide
195..242
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 polyA_site
2518..2532
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                                           2352..2357
                                                       polyA_site
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1831..1836
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US-08-232-463-14
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; ORGANISM: Homo sapiens
US-09-180-100-16
                                                                                                                                                                                      Patent No. 5670367
GENERAL INFORMATION:
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                                                                                                                                                                                                              Sequence 14, Application US/08232463 Patent No. 5670367
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CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 129; Conservative
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GENERAL INFORMATION:
    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
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STREET: 1800 Dia
CITY: Alexandria
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5.4%; Score 129; DB 4; Length 2534;
Local Similarity 100.0%; Pred. No. 2e-25;
hes 129; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4%; Score 129; DB 4; Length 2534; 100.0%; Pred. No. 2e-25; rative 0; Mismatches 0; Indels (
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ETLING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.76
1432 YYYGTACCAAATTCT 1446
                                              363 tgtctattagatgct 377
                                                                       303 atttgcagagataatacagagaatgcccatataccatcctccttatcccacttctttttg 362
                                                                                                                                                                                                                                                                        243 ttttacatttttttatttaaatgaacttttcattttggaatagttttaggatttcaaaaa 302
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LENGTH: 7218 base pair
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                 63 ctataatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataattc 122
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MEDIUM TYPE: Floppy disk
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TELEFAX: 899149
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3.0%; Score 71.8; DB 1; Length 7218;
Local Similarity 1.9%; Pred. No. 1.5e-09;
hes 7; Conservative 238; Mismatches 130; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       3 cttttttggctacatttttttatttgtaaagtaagtttaataatcactcatctcactggg 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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US-08-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367

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INFORMATION FOR SEQ ID NO: 14:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                     COUNTRY:
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480 ggtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaa 539
                                                                                                                                                                                                                                                                                  420 tggcactaacagtctactgaaaggtggaacagagacaagcctatcaacacctacaagact 479
                                                                                                                                                                                                                                                                                                                                                360 ttgtgtctattagatgctcagagtgtgtgcacaaggctggcacgcccagggtcttcctca 419
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APPLICATION NUMBER:
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                            660 taattgggaagggagagagttgcagagtgaggtgcagagcttggtggacgatgccaaag 719
                                                                                           600 ctgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatc 659
                                                                                                                                                        540 cctaacctagatttgagggcccaaacaggctccagaagaaaatgtcaactgagaggaagc 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                  2.8%; Score 67.4; DB 1;
ilarity 8.0%; Pred. No. 2.5e-08;
Conservative 228; Mismatches 174;
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US-08-836-022A-10
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; patent No. 6001557
                                                                                                                                                                                                                                                                                          US-08-836-022A-10
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                                                                                                                                                                                                                                         Query Match
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                                                                                                                                   16048 CCGGCCGCCTGCAGCTGGCCCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGA 16107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chen, Shu-Jen
APPLICANT: Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
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                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780 gatgtcattatccaaac 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 28-OCT-1994
16168 TTTACAACGTCGTGACTGGGAA 16189
                                                                                                                                                                                                                                                                                                            TOPOLOGY: ur
                                                                                                                                                                  1667 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 1726
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                              1787 gggaccccggttggagagagga 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: Z15 -540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bak, Mary E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                     Watch 2.7%; Score 63.6; DB 3; Length 19307; Local Similarity 65.5%; Pred. No. 4.6e-07; Nes 93; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1947
                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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Fisher, Krishna J.
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                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                             CDNA
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; Sequence 3, Application US/08836022A
; Patent No. 6001557
                                    RESULT 11
US-08-836-022A-3/c
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APPLICATION NUMBER: 08/836,022
FILLING DATE: CUNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
TELEPHONE: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-427-048A-10
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                                                                                                                                                                                    16108 GCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGT 16167
                                                                                                                                                                                                                                                                    16048 CCGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGA 16107
                                                                                                                 16168 TTTACAACGTCGTGACTGGGAA 16189
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GENERAL INFORMATION:
                                                                                                                                                   1787 gggaccccggttggagagagga 1808
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                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/427,048A FILING DATE: 21-Oct-1999 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Trustees of the University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Spring House Corporate Cntr, P O Box 457 CITY: Spring House STATE: Pennsylvania COUNTRY: USA
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Fisher, Krishna J.
Chen, Shu-Jen
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US-09-427-048A-3/c
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                              1788 ggaccccggttggagagagga 1808
                                                                                                                                                                                                                                                                                                                                                  1728 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggaggg 1787
                                                                                                                                                                                                                                                                                                                            2920 CTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                                                                                                                                                                                                                                                                                                                   2980 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 2921
                                                                                                                                                                                                                                                                                                                                                                                                                           1668 ctgaggccagccctggctgccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
                                                                                                                                                                                                                                                                2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
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FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SAPPLICATION NUMBER: US/08/836,022A
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Trustee M.
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
Chn-Jen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Weitzman, Matthew TITLE OF INVENTION: Improved Adenovirus Virus and NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 215-540-5818
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             TITLE OF INVENTION: Improved Adenovirus Virus and
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                                                                                                   APPLICANT: Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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                                   Weitzman, Matthew
                                                         Chen, Shu-Jen
                                                                     Wilson, James M.
Fisher, Krishna J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Score 62.6; DB 3; Length 9972; 65.2%; Pred. No. 6e-07; ative 0; Mismatches 49; Indels 0
Methods of Use Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
                                                                                                                                                                                         APPLICANT: Camero
APPLICANT: Shaw,
                                                                                                                   APPLICANT: Cameron, Douglas C. APPLICANT: Shaw, Anita J. APPLICANT: Altaras, Nedim E. TITLE OF INVENTION: MICROBIAL PROTITLE OF INVENTION: FROM SUGAR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                          1668 ctgaggccagccotggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2980 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCCCGGACATGTACAGAG 2921
                                                                                                                                                                                                                                                                                                                                                                                        1788 ggaccccggttggagagagga 1808
                                                                                                                                                                                                                                                                                                                                                        2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10
                                STATE:
                  COUNTRY:
                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
RY: U.S.A.
53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-540-5818
                                                      Madison
                                WH
                                                                    E: DeWitt Ross & Stevens S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.2%;
                                                                                                                                                         MICROBIAL PRODUCTION OF 1, 2 PROPANEDIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Pred. No. 6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; | Indels 0; Gaps
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNP
MYPOTHETICAL: NO
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1668 ctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cameron, bou
APPLICANT: Shaw, Anita
APPLICANT: Altaras, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/498,599
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 582
           ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%;
Local Similarity 75.0%;
Local Similarity 75.0%;
Local Similarity 75.0%;
Local Similarity 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 53717-1914
                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                  CITY: Madison
                                                                                                                                                                                                                                                                                                 STREET:
                                                                     CLASSIFICATION:
                                                                                     FILING DATE:
                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                 Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608-831-2106
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                                                                                                                                                                                                                                                                                                  E DeWitt Ross & Stevens S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circular
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cameron, Douglas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector pSE380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                      1,2-PROPANEDIOL FROM SUGAR
                                                                                                                                                                                                                                                                                                                                                                                          MICROBIAL PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                           Nedim E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62.4; DB 3; Length 4476; pred. No. 4.4e-07; 0; Mismatches 26; Indels 0;
                        09820.037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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0,

TELEPHONE:

608-831-2100 608-831-2106

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US-08-306-691B-19
                             IELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-306-691B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Vector pse380
US-09-498-599-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08306691B Patent No. 5734039
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US, FILING DATE: September CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                  NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SKOTSKI, TOMASZ
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1728 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctt 1771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1668 ctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPULLUE: DN. MOLECULE TYPE: DN.
                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583 CTCGAGAACTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTT 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 2.6%; Score 62.4; DB 4; Length 4476; Local Similarity 75.0%; Pred. No. 4.4e-07; nes 78; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calabretta, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PS/2
                                                                                                                                                                                                                                                                                                                                                          September 15, 1994
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                            US/08/306,691B
                                                                                                                                                                                                              8321-8
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                                                                                                                           В
                                                                                                                                                    Qγ
                                                                                                                                                                                    В
                                                                                                                                                                                                                             Query Match 2.5%; Score 59.8; DB 1; Length 35100; Best Local Similarity 55.6%; Pred. No. 6.9e-06; Matches 115; Conservative 0; Mismatches 92; Indels 0;
3986 TTCTTTCTTTTTCTATCTTTTGAGA 4012
                                                 3806 GAGGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTAGGCGACAGAGCAAGACT 3865
                 267 acttttcattttggaatagttttagga 293
                                                                                                                         207 teettteetteeeteacacceetttteetteettetttttacatttttttatatttaaatga 266
                                                                                                                                                                                              87 gaagatccacatatgtgagttgctggcttataattcacactcaagagatactgattttgt 146
                                                                                                                                                                                                                             0; Gaps
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Search completed: September 7, 2002, 18:26:08 Job time: 29062 sec

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                September 7, 2002, 22:32:06; Search time 13836.9 Seconds (without alignments) 3721.275 Million cell updates/sec
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2380
1 agcttttttggctacatttt......tggctaatcaaagagacgtg 2380
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11:
12:
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25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pending_Patents_NA_Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
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76: /cgn2_6/ptodata/2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2380 1923.4 11899.6 17713.4 17713.4 1772.8 1372.8 1372.8 1372.8 1372.8 6170.6 6170.6 6296.8 296.8 296.8 296.8 296.8 296.8 239.2 239.	Score
100.0 100.0 100.8 179.8 179.0 172.0 172.0 172.0 172.0 172.0 173.7 174.8 117.8 11	Query Match L
2380 2897 3212 2165 2165 21668 1608 1608 1608 1608 2814 449 449 449 458 458 2871 2871 2871 2871 2871 2871 2871 287	Length D
332 332 332 332 332 332 332 332 332 332	DB
US-09-834-291-3 US-09-834-291-1 US-09-997-722-10 US-09-802-669-94 US-09-802-669-94 US-09-802-669-94 US-08-377-522C-1 US-08-377-522C-1 US-08-377-522C-1 US-08-377-522C-1 US-08-377-522C-1 US-09-404-284-674 US-09-924-038-674 US-09-924-038-674 US-09-925-214-682 US-09-925-214-682 US-09-925-214-8816 US-09-726-172-2083 US-09-726-175-3031 US-09-726-175-3031 US-09-726-175-3031 US-09-726-188-5939 US-09-726-810-2456 US-09-760-455-21 US-09-760-455-21 US-09-760-455-21 US-09-780-455-21 US-09-780-5881-187 US-09-987-618-11167 PCT-USU0-05883-187 US-09-958-475-120	ID
Sequence 1, Appli Sequence 10, Appli Sequence 11, Appli Sequence 94, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 674, App Sequence 674, App Sequence 14682, A Sequence 14682, A Sequence 3367, Ap Sequence 3367, Ap Sequence 3915, Ap Sequence 2013, App Sequence 2013, App Sequence 21, Appl Sequence 327, App Sequence 327, App Sequence 15844, A Sequence 1187, Ap Sequence 1187, Ap Sequence 1187, Ap Sequence 1187, Ap Sequence 1187, Ap Sequence 187, App Sequence 1187, Ap	3

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Sequence 3. Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-834-291-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-834-291-3
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 2380
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
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GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION UNBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
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PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
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NUMBER OF SEQ ID NOS: 32
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US-09-997-722-10
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
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CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
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APPLICANT: MotTis, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
                                              8441 agottttttggctacatttttttatttgtaaagtaagtttaataatcactcatctcactg 8500
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; TYPE: DNA
; ORGANISM: Homo Sapiens
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE9/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
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Best Local
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APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marcusson, Eric G.
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                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (1782)...(1813)
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                    181 ccttccattccttcccttacctctcctttccttccctcacacccccttttccttcctt
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                                                                                                                                                                                                                                                                                       Y Match 72.0%; Score 1713.4; Local Similarity 99.9%; Pred. No. 0;
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GENERAL INFORMATION:
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                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sertich, Gary J.
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
                                                                                        SEQUENCE CHARACTERISTICS:
           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: I
STATE:
FEATURE:
                                                                                                                                                                               NAME: Sertich, Gary J. REGISTRATION NUMBER: 34. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-377-522-1

NAME/KEY: LOCATION:

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1100 tecattecaggaacgtetgtgageeteteatgttgeageeacaacatggaeageeeagte 1159
                                                                                             1160
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                                                                                                                                                                                                                                                                                                                                                                                                   487
                                                                                                                                                                                                                                                                                                                                                                                                                                          427 TGTCCAGTCTGGAACTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 739
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                                                      AAATGCCCCGCAAGTCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCA
                                                                    aaatgccccgcaagtctttctctgagtgactccagcaattagcccagggctcctgtaccca 1219
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                                                                                                            TCCATTCCAGGAACGTCTGTGAGCCTCTCATGTTGCAGCCACAAGATGGACAGCCCAGTC 846
                                                                                                                                                                  GGGCCCTCCCTTTTCAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTG
                                                                                                                                                                                                                      GGCTATGCGATTTGGCTTAAGTTGTTAGCTTTGTTTTCCTCTTGAGAAATAAAAACTAAG
                                                                                                                                                                                                                                                                            GGCCAGGAAATAATGAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGG
                                                                                                                                                                                                                                     99cta19cga1ttggcttaagttgttagctttgttttcctcttgagaaataaaaactaag 1039
                                                                                                                                                                                                                                                                                                                                                                                    CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG 859
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99.4%;
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                                                                                         TELEFAX: (713) 777-69
INFORMATION FOR SEQ ID NO:
             TOPOLOGY: 1
MOLECULE TYPE:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
                                                                                                                                                                                                                      APPLICATION NUMBER: [FILING DATE: January CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      STATE: TX
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Human Fas Gene Promoter Region NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1700 gcctcttctcccgcgg 1715
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                                 TYPE: nucleic acid
STRANDEDNESS: doub
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                      linear
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genomic DNA
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                                  double-stranded
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IMMEDIATE SOURCE:
LIBRARY: (FIXII; EMBL-SD6/T7
CLONE: FIX1, FIX2, FIX3; EMBL
POSITION IN GENOME:
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ORIGINAL SOURCE:
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Local Similarity 99.4%;
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                                                                                                                                                              CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG
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tccattccaggaacgtctgtgagcctctcatgttgcagccacaacatggacagcccagtc 1159
                                                                            GGCTATGCGATTTGGCTTAAGTTGTTAGCTTTGTTTTCCTCTTGAGAAATAAAACTAAG
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Pred. No. 2.1e-285;
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                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
                                                                       FILING DATE: January CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                        SOFTWARE: Microsoft WC CURRENT APPLICATION DATA:
             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                           STREET: 801
CITY: Houst
STATE: TX
ZIP: 77071
                                                                                                                                               COMPUTER: Apple Macintosh OPERATING SYSTEM: Macinto
                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                ADDRESSEE:
                                                            APPLICATION NUMBER:
                                                                                                           APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaactacagcagaagcctttagaaagggcaggaggccggctctcgaggtcctcacctgaa 1339
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                                                                                                                                                                                                                                     Houston
                                                                                                                                                                                                                                                 E: Benjamin Aaron Adler,
8011 Candle Lane
                                                                                                                                                                                                                                                                                                             Mountz et al.
                                                                                                                                      Microsoft Word for Macintosh
                                                                                                 January 20, 1995
                                                                                                                                                                                                                                                                                                   Human Fas Gene Promoter Region
                                                                                                                                                    Macintosh
                                                                                                                 US/08/377,522D
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            607
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INFORMATION FOR SEQ ID NO:
                                                                                                               487
                                                                                                                                                                 427
                                                                                                                                                                                                                   680 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 739
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LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMB
                                                                                                                                                                                                                                                                                                            247 CCAAACAGGCTCCAGAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGC
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ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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STRANDEDNESS: doub
TOPOLOGY: linear
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GGCCAGGAAATAATGAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGG
          99cca99aaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg 979
                                                               LENGTH:
                                                                                                  CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG
                                                                                                                ccttctgtaaaattcatgctaaactacctaagagctatctaccgttccaaagcaatagtg
                                                                                                                                                                                                      TTGCAGAGTGAGGTGCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTG
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ORGANISM: Homo sapiens

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                                                                                     Sequence 29531, Application US/60324185
GENERAL INFORMATION:
APPLICANT: MORTIS, MacDonald
APPLICANT: Lalp, Preeti
APPLICANT: Lolep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1 p
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CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 29531
LENGTH: 3814
TYPE: DNA
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US-09-834-291-2
Sequence 2, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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OTHER INFORMATION: Incyte ID No: 415714.1
TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122 CURRENT EPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: PCT/DE99/03343 PRIOR FILING DATE: 1999-10-18 PRIOR APPLICATION NUMBER: DE 198 47 779.1
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Pred. No. 2e-141;
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Sequence 674, Applicat GENERAL INFORMATION: GENERAL INFORMATION: ITITLE OF INVENTION: ICURRENT APPLICATION ICURRENT FILING DATE: CURRENT FILING DATE: NUMBER OF SEQ ID NOS SOFTWARE: Hy-patent.] SEQ ID NO 674

LENGTH: 449

APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 20411-780
CURRENT APPLICATION NUMBER: US/09/404,284
CURRENT FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 674

US-09-404-284-674/c

Sequence 674, Application US/09404284

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; TYPE: DNA
; ORGANISM: HOMO
US-09-834-291-2
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SEQ ID NO 2
LENGTH: 720
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aatcaaagagacgtg 720
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Sequence 674, Application US/09524038
GENERAL IMFORMATION:
APPLICANT: Dimenac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Ones, Lee w.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obt
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 780CIP
CURRENT APPLICATION NUMBER: US/09/524,038
CURRENT FILING DATE: 2000-03-13
EARLIER APPLICATION NUMBER: 09/404,284
EARLIER FILING DATE: 1999-09-21
NUMBER OF SEO ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
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                                                                                           Query Match
                                                                                                                                                                                                         SEQ ID NO 674
                                                                                                                                                  LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
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1233 cgctctgagctccattctccttcaagacctccccaacttcccaggttgaactacagcaga 1292
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                                                                         V Match 17.8%;
Local Similarity 99.3%;
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                                                            426;
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                                                          Conservative
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99.3%;
                                                       0; Mismatches
                                                               Score 424.2; DB 19; Length 449; Pred. No. 6.1e-81;
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Pred. No. 6.1e-81;
0; Mismatches 3; Indels 0;
                                                     3; Indels
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; ORGANISM: Homo sapiens
US-09-306-350A-14682
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APPLICANT: Dickson, Mark C.

APPLICANT: Drmanac, Radoje T.

APPLICANT: Jones, Lee W.

APPLICANT: Jones, Lee W.

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

TITLE OF INVENTION: From Various cDNA Libraries

FILE REFERENCE: 20471-776
                                                                                                                                                                                                                                                                                            Matches 391;
                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                             Query Match
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280 GCAGAGCTTGGTGGGCGATGCCAAAGGAATACTGAAACCTTTAG-GTGTCCAGTCTGGAA
                  694 gcagagcttggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctggaa 753
                                                                                       634 ttaatgtgttattaattgggttgaatctaattgggaagggagagggtgcagagtgaggt 693
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                                                                   TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGA-GTTGCAGAGTGAGGT
                                                                                                                                        GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGT-GGCTAAGCAAAGGGTTA
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Pred. No. 2.3e-58;
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APPLICANT Jones, Lee W.

APPLICANT Labat, Ivan
APPLICANT Labat, Ivan
APPLICANT Stache-Crain, Birgit
APPLICANT Stache-Crain, Birgit
TITLE OF INVENTION: Novel Nucletc Acid Sequences Obtained
TITLE OF INVENTION: From Various CDNA Libraries
FILE REFERENCE: 20411-776
CURRENT APPLICATION NUMBER: US/09/909,629
CURRENT FILING DATE: 2001-07-19
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: Pt_CT_1 Version 1.1
SEQ ID NO 14682
LENCTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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339 TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGTGTGCAGAGTGAGGT 281
                                                                162 CATGCTAAACTACGTAAGAGCTATCTACCGTTCCAAAGCAATAG-GACTTTGAACAGTGT 104
                                                                                    814 catgctaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagtgt 873
                                                                                                                                                   754 ctgcatccaaattcaggttcagtaatgatgtcattatccaaacataccttctgtaaaatt 813
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                                                                                                                                     Drmanac, Radoje T.
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Search completed: September 7, 2002, 22:33:42 Job time: 43916 sec

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GENERAL INFORMATION:
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| 1107 ctttcttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctg 11080
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CURRENT FILING DATE: 2001-12-06

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21

SOFTWARE: Hy-patent.pl Version 3.1

SEQ ID NO 674

TENCTH- 469
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US-10-011-154-674
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APPLICANT: Labat, Ivan
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Best Local S
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Match 17.8%; Score 424.2; DB 7 Local Similarity 99.3%; Pred. No. 7.2e-81; Local Similarity 19.3%; Pred. No. 7.2e-81; Pred. No. 7.e-81; Pred. N
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PRIOR APPLICATION NUMBER: 60/180.628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-09-26
PRIOR PAPPLICATION NUMBER: 60/220,963
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-08-14
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ16C1N
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/211,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1653 ggcacggaa 1661
                                                                                                                                                                 US-10-211-364-477
                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 477
                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1778
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                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 GGCACGGGA 21
                                                                                                                    Query Match
                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                           Matches
                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (593)
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (594)
                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                  LOCATION: (704)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                              NAME/KEY: misc_feature
                             1537 tcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacgcttctg 1596
                                                                                                        Local Similarity
                                                                                                Conservative
                                                                                                                      10.0%;
                                                                                                        0; Mismatches
                                                                                                                      Score 237.4; DB 6; Length 772; pred. No. 6.2e-41;
                                                                                                                  1; Indels 0; Gaps
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PCT-US02-10824-85
                                                                                                                                RESULT
    Sequence 85, Application PC/TUS0210824

APPLICANT: OriGene Technologies

TITLE OF INVENTION: Prostate Cancer Expression Profiles

CURRENT APPLICATION UMBER: PCT/US02/10824

CURRENT FILING DATE: 2002-04-08
                                                                                            Sequence 85,
                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: n equals a,t,g, or c US-10-143-906-21
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                            1657 cggaacacacctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 1715
                                                                                                                                                                                                1597 gggagtgagggaagcggtttacgagtgacttggctggagcctcagggggcggggcactggca 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-143-906-21
                                                                                                                           189 cggaacacacctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 247
                                                                                                                                                                                                                                                      1537 tcgtgagctcgtcttgatctcgcgcaagagtgacacacaggtgttcaaagacgcttctg 1596
                                                                                                                                                                                  129 gggagtgägggaagcggtttacgägtgacttggctggagcctcäggggcgggcactggca 188
                                                                                                                                                                                                                                                                                                            1477 ccccaacccgggcgttccccagcgaggcttccttcccatcctcctgaccaccggggcttt 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n equals a,t,g, or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/143,906
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (594)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ70C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (593)
                                                                                                                                                                                                                                       69 togtgagctogtototgatotogogcaagagtgacacacaggtgttcaaagacgcttotg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                             9 cgccaacccgggcgttccccagcgaggcttccttcccatcctcctgaccaccggggcttt 68
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
2002-04-08
                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 237.4; DB 7; Length 772;
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APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
APPLICANT: SASAI, Hitoshi
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, Iwao
TITLE OF INVENTION, Jun
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
PRIOR APPLICATION NUMBER: US 60/311,837
EVENTAME: APPLICATION NUMBER: US 60/311,837
SOFTMARE: PACE DINOS: 1346-14
SOFTMARE: PACE DINOS: 1346-15
SEQ ID NOS: 1346-16
SEQ ID NOS: 1346-16
SEQ ID NOS: 1346-17
TYPE: DNA
                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Genbank Accession No. X63717
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                             Query Match
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                1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
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GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
                                                             1561 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 1620
121 tggctgcccaggcggagctgcctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENURAL INFORMATION:
APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US02-10824-85
                                            61 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc
                                                                                                    f 1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                  Local Sim
hes 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/281,732
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/281,731
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                            Similarity
                                                                                                                                                                              ilarity 100.0%; Pred. No. 3.2
Conservative 0; Mismatches
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Similarity 100.0%; Score 155; DB 1; Length 2551;
55; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                        6.5%; Score 155; DB 1;
100.0%; Pred. No. 3.2e-23;
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APPLICANT: ENGELIAND, ERIC
APPLICANT: ENGEL COMPOSITIONS AND METHODS FOR CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TITLE OF INVENTION: NOVEL COMPOSITION OF STATE
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-20
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SEQ ID NO 1263
SEQ ID NO 1263
LENGTH: 2551
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Sequence 1263, Application US/10035832
GENERAL INFORMATION:
GAPPLICANT: MOTILS, David
APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1263
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CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 143
LENGTH: 2551
TYPET DATE:
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US-10-007-926A-143
Sequence 143, Application US/10007926A
GENERAL INFORMATION:
GENERAL INFORMATION:
FRANCOIS
APPLICANT: BERTUCTIF DENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.5%; Score 155; DB 6; Length 2551; Best Local Similarity 100.0%; Pred. No. 3.2e-23; Antches 155; Conservative 0; Mismatches 0; Indels
                                                                                              US-10-007-926A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES FILE REFERENCE: 1546-R-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VIENS, PATRICE APPLICANT: FERT, VINCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                 OTHER INFORMATION: tumor necrosis factor receptor superfamily, OTHER INFORMATION: member 6 (INFRSF6) gene.
                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                ORGANISM: Homo sapiens
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BIRNBAUM, DANIEL
NGUYEN, CATHERINE
             100.0%;
                                  6.5%;
          Score 155; DB 7;
pred. No. 3.2e-23;
                                            Length 2551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-053-375B-233
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 233
LENGTH: 2534
                                                                                                                                                                                                                                                                                                                                                  US-10-035-832-1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
5.4%; Score 129; DB 5; Length 2534;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 129; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                ; GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-08-31
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APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
                                                                            PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1259
SEQ ID NO 1259
                                                                                                                                                                                                                                                                                                                               Sequence 1259, Application US/10035832
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                                                                                                                                                                                                                                           APPLICANT: MOTRIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1647
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                                                     TYPE: DNA
NAME/KEY: misc_feature
                                  ORGANISM: Mus musculus
                                                                  LENGTH: 55996
                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                        US-10-027-632-145670/c
; Sequence 145670, Application US/10027632
; GENERAL INFORMATION:
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; LOCATION: (55549)..(55568)
; OTHER INFORMATION: "n" at positions 55549 thru 55568 can be any base
US-10-035-832-1259
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 68.2; DB 6; Length 55996; Best Local Similarity 63.6%; Pred. No. 0.00024; Matches 152; Conservative 0; Mismatches 83; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7917 agacttetetttttgatagatttatateetgaetatggteeeetaaetetttteaeeee 7975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7859 aag-gaggaagtaataatgtet-aacacagcaggtgagggttttecettttaetgaaaat 7916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7799 cagtaaagaagtataagaattttttttaacgaaaattggtcaggaaataatccgtaacaa 7858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (53136)..(53155)
OTHER INFORMATION: "n" at positions 53136 thru 53155 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943 aggacaggaagtaattgtgaatgtttaatatagctggggctatgcgatttggcttaagtt 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (50692)..(50711)
OTHER INFORMATION: "n" at positions 50692 thru 50711 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  883 cacgaaagaattacaagatttttttttaaagaaaattggccaggaaataatgagtaacga 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (50692)..(50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (48271)..(48290)
OTHER INFORMATION: "n" at positions 48271 thru 48290 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           825 acctaagagctatctaccgttccaaagcaatagtgactttgaacagtgttcacca--gag 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (46987)...(47006)
OTHER INFORMATION: "n" at positons 46987 thru 47006 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: (48271)..(48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (42691)..(42710)
OTHER INFORMATION: "n" at positions 42691 thru 42710 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (31023)..(31239)
OTHER INFORMATION: "n" at positions 31023 thru 31239 can be any base
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OTHER INFORMATION: "n" at positions 29253 thru 29272 can be any base
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US-10-113-872-1669/c
; Sequence 1669, Application US/10113872
; GENERAL INFORMATION:
                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                      Db
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                      APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert ,
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-113-872-796/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human US-10-027-632-145670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 796, Applic GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/113,872 CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICAMY: Fanger, GATY R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
                                                                                                                                                        2374 TAGATTTACAGAGAAGTTGCAGAGATAGTACAAAGAGTTCCTGTATACCCCTTCACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                         2434 Tritititititititititititititititaaattaaattaaactitiaattitiggaatgatac 2375
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145670
LENGTH: 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                             289 taggatttcaaaaaatttgcagagataatacagagaatgcccatataccatcctcc 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2435
                                                                                                                                                                                                                                           229 ttttccttccttcttttacatttttttatttaaatgaacttttcattttggaatagttt 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                            Y MACCH 2.5%;
Local Similarity 69.8%;
hes 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 TGTTTTGTTTAAATAAACTTTTGCTTTTAGAACAGTTTTAGCTCTACAGAATTATTGCA 248
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Local Similarity 69.2%; Pred. No. 0.0031;
Length 816;
Mismatches 37; Indels
Henderson, Robert
Kalos, Michael D.
Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
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Vedvick, Thomas S.
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10113872
                                   Robert A.
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                    Score 60; DB /; Pred. No. 0.0061; Viematches 35; Indels
                                                                                                                                                                                                                                                                                                                                DB 7; Length 2435;
                                                                                                                                                                                                                                                                                                 0;
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APPLICANT:

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; TYPE: DNA; ORGANISM: Homo sapiens
US-10-113-872-1669
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US-10-027-632-91808
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1669
LENGTH: 2821
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APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                       ; ORGANISM: Human
US-10-027-632-91808
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91808
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR TILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y match 2.5%; Score 60; DB 7; Length 2821; Local Similarity 69.8%; Pred. No. 0.0063; | Local Similarity 69.8%; Arches 25.
                                                           310 gagataatacagagaatgcccatatacc 337
                                                                                                                                             Local Similarity es 70; Conserv
                                                                                                                                                                                                                                                                                                                           542
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                                                                                                                                                    Conservative
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                                                                                                                                                                           2.5%;
                                                                                                                                                           0; Mismatches
                                                                                                                                                                             Score 59.2; DB 7; Length 542; pred. No. 0.0062;
                                                                                                                                                           18; Indels
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                                                                                                                                                                       0;
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Search completed: September Job time: 37198 sec

8, 2002, 01:12:00

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RESULT 15
US-10-027-632-304597
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; ORGANISM: Human
US-10-027-632-304597
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 304597
LENGTH: 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                            Ouery Match 2.5%; Score 59.2; DB 7; Length 542; Best Local Similarity 79.5%; Pred. No. 0.0062; Matches 70; Conservative 0; Mismatches 18; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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                                                                               310 gagataatacagagaatgcccatatacc 337
Application US/10027632
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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No.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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294.4

294.4

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253.6

185.2

181.8
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1: em
2: em
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2380
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Copyright (c) 1993 - 2000 Comp
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first 45 summaries
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BI763679 603049567
AA058563 zf55b04.s
AA058275 zf53g03.s
AA012028 ze34d02.s
AA047220 zf49e11.s
AA027918 zf59h03.s
AA027992 ze65f07.s
AA020992 ze65f07.s
H84298 ys95e09.s1
H86126 ys94g08.s1
AA018441 ze50a08.s
H86544 yt04f01.s1
R85827 yq22g10.s1
AV715411 AV715411
BIRS827 603083875
AW239285 xb38602.y
BG288747 602385566
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1 (bases 1 to 467)
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zj19h02.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:450771 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA704610.1 GI:2714528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA704610
                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:1387127"
                       /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:450771"
                                                                                                                                                                                             Location/Qualifiers
                                                                                          /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
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BIO45052 MR4-OT019
BIO45083 MR4-FT126
BG998195 MR4-FT126
BG997854 MR4-FT126
BG997854 MR4-FT126
BG99787 ARR4-HN005
AA521324 aa68e09.s
BG104597 MR4-HN005
AA521324 Aa68e09.s
BG998167 MR4-HT126
BG998167 MR4-HT126
BG998167 MR4-HT126
BG015436 RC2-GN035
BG918136 RC4-CI019
BF759346 RC4-CI019
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BH108582 MR4-MT033
ALIO6663 Drosophil
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGATTTGAGGGCCCAAACAGGCTCCAGAAGAAAATGTCAACTGAGAGGAAGCCTGAAGG
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tagatttgagggcccaaacaggctccagaagaaaatgtcaactgagaggaagcctgaagg 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaacctaacc 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAGTCTACTGAAAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACTGGTGGTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact nature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGAGATAATACAGAGAATGCCCATATACCATCCTCCTTATCCCACTTCTTTTTGTGTC 120
                                                                  Contact: Robert Strausberg, Ph.D
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                    603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5/
                                                                                                                                                         Eukaryota;
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Pred. No. 4.3
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                                                                                                                                                          2185 totetttettettttgeeetttettagettge 2216
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                                    AA058563 603 bp mRNA linear EST zf55b04.sl Soares retina N2b4HR Homo sapiens cDNA clone
                           IMAGE: 380815 3', mRNA sequence.
AA058563.1 GI:1551370
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pCWV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
stomachs, 62 yo male colon; 46 yo male kidney, and pool of 2
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
023. Note: this is a NH_MGC Library."
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/clone="IMAGE:5189752"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 921 Std Error: 0.00 seq primer: -40M13 fwd. from Amersham | High quality sequence stop: 467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                         TACTCGTTCCCACCGCACAGAACCCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT 240
                                                        tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 2320
                                                                                                                                                                                                                                                                                                                                     299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:380815"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GDB:1289072"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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142 c 140 g 175 t
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                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Score 298.4; DB 9; Length 603; Pred. No. 2.3e-43;
                                                                                                                                                                                                                                                                                                                                               1; Indels
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1 (bases 1 to 577)
Hillier L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Parsons, J., M., Hultman, M., Kucaba, T., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Lennon, F., Trevaskis, E., Waterston Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R., R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE: 380692 3', mRNA sequence.
AA056275
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 178.
                                                                                                                                                                                                                                                                  double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7773 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 Caucasian and total removal. The retinas RNA was kindly hrs after their removal. The retina RNA was kindly hrs after their removal. The retina RNA beak kindly solved by Roderick R. McInnes M.D. ph.D. from the provided by Roderick R. McInnes M.D. ph.D. from the solves and M.Fatima Bonaldo.

Soares and M.Fatima Bonaldo.

135 g 163 t 11 others
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                                                                                                                                                                 Conservative
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/clone="IMAGE:380692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:1288949"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="55
                                                                                                                                                                                      12.4%;
98.3%;
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                      Score 294.4; DB 9; Length 577; pred. No. 1.2e-42;
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2261 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 2320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCANAGAGACGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TACTCGTTCCCACCGCACAGAACCCGGNGCCTATTATTGGGCCAAGAAACTTGAGCAGCCT 240
                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: mob.REGA+ET High quality sequence stop: 372.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashU-Merck EST Project

The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                                      /dev_stage="55 year old"
                                                                                                                                                                                                                                                                                   /tissue_type="retina"
                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                          /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:360867"
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:1277412"
                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
     12.0%;
                                                                                                                                                                                                                                                                                                                                                                                              on/Qualifiers
Score 286.4; DB 9
Pred. No. 3.2e-41;
                                                                   103 g
                                                                   138 t
          DB 9; Length 442;
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                                                                                                                                                                                                                                                                         High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                            Insert Length: 893 Std Error: 0.00
Sed primer: -40Ml3 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
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/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="0rgan: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:1288557"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
                                                                                                               /sex="male"
                                                                                                                   /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                        Location/Qualifiers
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                                                          FEATURES
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44/ DP MKNA LINEAL TO Zf59h03.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381269 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                               Unpublished (1995)
                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 447)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA057418.1 GI:1550059
                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                        High quality sequence stop: 339.
Location/Qualifiers
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a 128 c 125 g 158 t 5 others
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/db_xref="GDB:1289526"
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ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:363877 3' similar to contains Alu repetitive element;, mRNA
Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Hilser, L., Lennon, G., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., B., Morris, M., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 to 467)
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//note="Organ: eye; Vector: pT/T3D (Pharmacia) with a /note="Organ: eye; Vector: pT/T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st modified polylinker; Sitehal Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primer [5', str
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                                                                                                                                  242 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCA 279
                                                                                                                                                                                       182 TACTCGTTCCCACCGCACAGAACCCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT 241
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                                                                                                                                                                                                                                                                                                                                                                                2 GTCACACAGAAAAAGAAACTGCCTTGTCTCCCTTTCCGGGAATTCTCTCTTTAAGACTGTA 61
                                   ys95e09.s1 Soares retina N2b5HR Homo sapiens cDNA clone
                                                               H84298
                       IMAGE:222568 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 833 Std Error: 0.00
Seq primer: 40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares and M.Fatima Bonaldo.
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/clone="IMAGE:363877"
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99.6%;
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Pred. No. 1.9e-39;
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                  2291 ctattattggccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgcc 2350
                                                                                                2231 ttetgettggteteetggtgggttggtggtactegtteeeacegcacagaaceeggege 2290
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181 CTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCC 240
                                                                           121 TICTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAGAACCCGGCGC 180
                                                                                                                                                         61 TGTTTTTCTGCCCTTCTCTTTCTTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGAT 120
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                                                                                                                                                                                                                                                                                                                                  270;
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Location/Qualifiers
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project
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High quality sequence stops: 364
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Fax: 314 286 1810
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Contact: Wilson RK
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                              2106 gtctcccttccgggaattctctctttaagactgtaagtcgctgc¢tgagtggtttcattt 2165
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ys94g08.s1 Soares retina N2b5HR Homo sapiens CDNA clone
IMAGE:222494 3', mRNA sequence.
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The WashU-Merck_EST Project
                                                                                                       270;
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Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 925 Std Error: 0.00
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Contact: Wilson RK
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/clone="IMAGE:222494"
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/db_xref="GDB:3851255"
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/lab_host="DH10B (ampicillin_resistant)"
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
     59 a
double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:362390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:1279093"
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                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares retina N2b4HR"
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ORIGIN

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2263 ctcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcctgt 2322
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Local Similarity 99.6%;
                                                                                                                                                                                                                                                                                                 High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 381)
1 (bases 1 to 381)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yt04f01.s1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:223321 3', mRNA sequence.
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/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:223321"
                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:3854355"
                                                                                                                               /sex="male"
                                                                                                                                             /clone_lib="Soares retina N2b5HR"
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Pred. No. 1.6e-35;
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mes 259; Conserv
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                               Email: estewatson.wustl.edu
Insert Size: 958
High quality sequence stops: 269
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 958
Std Error: 0.00
              Insert Length: 958 Std Error:
Seq primer: Promega -21m13
High quality sequence stop: 269.
                                                                                                                                                                                                                                                                               ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                     Washington University School of Medicine
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
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314 286 1810
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Location/Qualifiers
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101 g 116 t 3 others
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 Mismatches

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Pred. No. 2.2e-35;
"'Armatches 9; Indels
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                                                                                                      TITLE
                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                           2363 gctaatcaaagagacgtg 2380
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                                                                                                                                                                                                                                                                  696 bp mRNA linear EST 11-OCT-2
AV715411 DCB Homo sapiens cDNA clone DCBAUÇ01 5', mRNA sequence.
AV715411
                                                                                      ,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
                                                                                                                              1 (bases 1 to 696)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                       AV715411.1 GI:10796928
           201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                               Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                              Homo sapiens
Email: hanzg@chgc.sh.cn
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/db_xref="GDB:3798432"
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/dev_stage="55_year old"
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/clone="IMAGE:274746"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 197; DB 10;
pred. No. 2.6e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         828 bp mRNA linear EST 04-OCT-2001 603083875F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222802 5', mRNA securence
                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                              High quality sequence stop: 813
                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                   Plate: LLAM11560
                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                namur
                                                                                                                                                                                                               http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
141 c 156 g 189 t
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/lab_host="BM25.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo
                                                                     /db_xref="taxon:9606"
/clone="IMAGE:5222802"
/clone_lib="NIH_MGC_120"
                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                            cocation/Qualifiers
                                                        /lab_host="DH10B"
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 Mismatches

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pred. No. 3.2e-23;
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Search completed: September 7, 2002, 14:51:47 Job time: 16206 sec
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                                                                                                                                                                                                                                                   2139 taagtogotgootgagtggtttcattttgtttttgtttttctgccc 2183
                                                                                                                         181 TTCTTACGTCTGTTGCTAGATTATCGTCCAAAAGTGTTAATGCCC 225
                                                                                                                                                                                                                                                                                                                                                                                                           male. Library is oligo-dT primed and directionally cloned (ECORY site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.75. Note: this is a NIH_MGC Library."
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OM nucleic - nucleic search, using sw model
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Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Result
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1: gb_ba:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

BASE COUNT	FEATURES Source	JOURNAL	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	Z	
/db xref="taxon:9666" /db xref="taxon:9666" 142 a 181 c 216 g 181 t	Location/Qualities 1. 720 //ramism="Homo Sapiens"	PATENT: DE 19847779-C 2 03-FEB-2000; PATENT: DE 19847779-C 2 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)	1 (bases 1 to 720) Mueller-Schilling, M., Krammer, P. and Oren, M. Movel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for cancer chemotherapy	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.	AX026090.1 GI:10187521	AX026090 720 bp DNA linear PAT 16-SEP-2000

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Matches Query Match

Local

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601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
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                                  Mueller Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 3212)
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Similarity 100.0%; Pred. No. 1.4e-158;
20; Conservative 0; Mismatches 0; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 187313)
                                               Homo sapiens
                                                                                                               Human DNA sequence from clone RP11-399019 on chromosome 10,
                                                                             HIG
                                                                                AL157394.15 GI:15384622
                                                                                                   complete sequence. AL157394
                                                                                                                                         AL157394
                                                              human.
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/db_xref="taxon:9606"
/84 c 809 g 84:
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FEATURES

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KEYWORDS ACCESSION DEFINITION AX026089

ORGANISM

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 144529 GAGGTGGGGTGGGGTGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC
                                                                                                                                                                        Db 144589 TGGAGGGGGACCCCGGTTGGAGAGAGGAGGGGAACTCCTGGACAAGCCCTGACAAGCCAA 144648
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                     61 gaggtgggggggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
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no Aug 31, 2001 this sequence version replaced gi:14161146.
On Aug 31, 2001 this sequence version replaced gi:142161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
Where differences are found these are annotated as variations
variation annotation may not be found in the sequence submission
variation annotation may not be found in the sequence with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least as compressions or more than one M13 subclone; and the one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following assembly was that the second of the confirmed by restriction digest. The following assembly was confirmed by restriction digest. The following assembly was that their source databases: Em: NMBL; Sw:, in the feature table with their source databases: Em: The Theorem of the confirmed by the confirm
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This sequence was finished as follows unless otherwise noted: all
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RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISSPROT; {\tt Tr:} , {\tt TREMBL} ; {\tt Wp:} , {\tt WORMPEP} ; {\tt Information} on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: pBACe3.6
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/note="Sequence confirmed by AC015461 sequenced by WIBR."
3 36398 c 36888 g 58358 t
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/clone="RP11-399019"
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Pred. No. 7.1e-157;
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Db 144829 CTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT 144888
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                                                1766 AAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGGGGAACTCCTGGACAA 1825
                                                                                                                             106 aagetttagggtegetggaggggaeceeeggttggagagaggageggaaeteetggaeaa 165
226 gcgggggcgggggagagagcctacagccttcagaacacatattgctcattttctggcagtt 285
                                                                 166 gccctgacaagccaaagccaaaggtccgctccggcgcgggttgggttgagttgcgcgccgcccc 225
                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                            Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 19847779-C 3 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE) Location/Qualifiers
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Mueller-Schilling, M., Krammer, P. and Oren, M.
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/db_xref="taxon:9606"
595 c 568 g 638
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99.7%;
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226 gcgggggcggggagagagcctacagccttcagaacacatattgctcattttctggcagtt 285
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1 (bases 1 to 2827)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy

Patent: DE 19847779-C 4 03-FEB-2000;

DEUTSCHES KREBSFRSCH (DE)
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/db_xref="taxon:9606"
676 c 657 g 766
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61 GAGGTGGGCGTGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 120
               61 gaggtgggggtgggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2753 AAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2693 TGCTGGGGTTGGTACTCGTTCCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAG 2752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2633 CTCTTTCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCC 2692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2573 CTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTTGTTTTTCTGCCCCTT 2632
                                                               1 GATCCCGCTGGGCAGGCGGGCAGCTCCGGCGCTCCTCGGAGGACCACTGCGCTCCACGTT
                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 aatcaaagagacgtg 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646 aaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2513 TTACCGTTTTTTATTGTCACACAGAAAAGGAAACTGCCTTGTCTCCCCTTCCGGGAATTCT 2572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2453 CGCCACCTTTTCTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGT 2512
                                                                               1 gatcccgctgggcaggcggggcagctccggcgctcctcgggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 tgctggggttggtggtactcgttcccaccgcacagaacccggcgcctattattggccaag 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 ctctttcttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcc 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 ctctttaagactgtaagtcgctgcctgagtggtttcattttgtttttgtttttcttgccctt 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2393 CTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAA 2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 ttaccgttttttattgtcacacagaaaggaaactgccttgtctcccttccgggaattct 465
                                                                                                                                                                                                                                                                                                                             Mueller Schilling, M., Krammer, P. and Oren, M. Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 32 03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggcaccttttcttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgt 405
[[]]]]]]]]]]]]]]]]]
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                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                        DEUTSCHES KREBSFORSCH
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32 from Patent DE19847779.
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                     /db_xref="taxon:9606"
72 c 110 g
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                      36.5%;
99.2%;
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                                                                                                                                                  Score 262.8; DB 6
Pred. No. 2.7e-51;
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                                                                                                                                       Mismatches
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                                         121 TGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCAA 180
                                                                                                                                                                                                              Local Similarity
                                  181
                                                                                              121
241 gagcctacagccttcagaacacatat 266
                                                                                                                   61
                                                                                                                             Homo sapiens DNA for enhancer of CD95 gene, partial AJ011034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD95 gene; enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                  GAGGTGGGCGTGGGGGGACAGGAATTGAAGCGGAAGTCTGGGGAAGCTTTAGGGTCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 266)
Mueller, M., Wilder, S., Bannasch, D., Israeli, D., Lehlbach, K.,
Li-Weber, M., Friedman, S.L., Galle, P.R., Stremmel, W., Oren, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                tggagggggaccccggttggagagaggggggaactcctgggacaagccctgacaagccaa 180
                                                                                                                                                                                                                                                                                                                                                                                                       p53 activates the CD95 (APO-1/Fas) gene in response to DNA damage
                                                                                                                                                                                                      264;
                                                                                                                                                                                                                                                                                                                                                                                              by anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 266)
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                     49
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                                                                                                                                                                                                                                                                                                   /gene="CD95"
159. .178
                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                             /evidence=experimental
                                                                                                                                                                                                                                                                                        /gene="CD95"
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:4165483
                                                                                                                                                                                                               36.5%; Score 262.8; DB 9; 99.2%; Pred. No. 2.7e-51; 0. Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pCR Profile:
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                                                                               270;
                                                                                         36.0%;
Similarity 99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                size: 150
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymerization:
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                                                                                                                                                                                                                                                                                                                                                                                           remplate:
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G27038
398 bp DNA linear STS 30-MAR-2
SHGC-30908 Human Homo sapiens STS genomic, sequence tagged site.
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Olivier, M. and Cox, D.R. (2000)
Unpublished, Olivier, M., Cox, D.R. (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Email: olivier@shgc.stanford.edu
Primer A: GTCTCCCTTCCGGGAATTCT
Primer B: AACCCCAGCAGGAGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Michael Olivier, David R. Cox
                                                                                                                                                                                                                                                                                                                                                         Prepared with primer pairs provided by Sandoz, derived from H86126
-- Washington University/Merck EST sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dNTPs:
each 200 uM
Tag Polymerase: 0.05 units/ul
motal Vol: 10 ul
                                                                                                                                                                                                        complement(132. .150)

93 c 105 g
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                     /clone_lib="Human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2nd Fl., Palo Alto, CA 94025, USA
                                                                                                          score 259; DB 1
pred. No. 2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5 mM
50 mM
20 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        each
                                                                                             Mismatches
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62 degrees C for 23 seconds
72 degrees C for 30 seconds
30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GCCCCTATTATTGGCCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                    Related sequences: D31968 x89101 AJ279011 AJ279013.
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muschen, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 702)
2 (bases 1 to 702)
3 (bases 1 to 702)
4 Muschen, M., Re, D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R. and Rajewsky, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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Muschen, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, K. and
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Apo-1 Fas; CD95 antigen; CD95 gene.
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                                     /gene="CD95"
                                                           /translation="MLGIWTLLPLV"
                                                                          /protein_id="CAC35540.1"
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282. .>313
                                                                                                                                  /standard_name="Apo-1 Fasi
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                                                                                                                               'codon_start=
                                                                                                                                                                                                                                       /standard_name="Apo-1 Fas"
                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Reed-Sternberg cells"
                                                                                                                                                                                                                                                                 /gene="CD95"
                                                                                                                                                                                                                                                                                               /gene="CD95"
                                                                                                                                                                                                                                                                                                     /note="Hodgkin's disease tissue-polymorphic allele (+275)"
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Submitted (19-SEP-2000) Muschen M., Department of Immunology,
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                    Related sequences: D31968 x89101 AJ279012 AJ279013.
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Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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Muschen, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, K. and
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                                          /gene="CD95"
/standard_name="Apo-1 Fas"
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      /standard_name="Apo-1 Fas"
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/standard_name="Apo-1 Fas"
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/note="Hodgkin's disease tissue"
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/db_xref="taxon:9606"
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100.0%; Pred. No. 2.1e-24;
tive 0; Mismatches 0;
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Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas),
1, polymorphic allele (+337).
AJ279013
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Apo-1 Fas; CD95 antigen; CD95 gene.
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Muschen, M., Re, D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R. and Rajewsky, K.

Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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                                                                                                                                                                                         Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                    Muschen, M.
Direct Submission
                                                                                                                                                                   Related sequences: D31968 X89101 AJ279011 AJ279012
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    /number=1 <1. .281
                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue-polymorphic allele (+337)"
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                                                               /gene="CD95"
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                          /standard_name="Apo-1 Fas"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                        submitted (28-JUN-1994) yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Faculty of Pharmaceutical Sciences; 13-1 Takara-mac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection J. Biol. Chem. 270 (30), 18007-18012 (1995)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2165)
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/db_xref="GI:13539243"
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                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
             /bound_moiety="NF-IL6"
772. .780
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                                                                                                                                                                                                                          /tissue_type="blood"
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                                                                                                              _moiety="NF-IL6"
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                                                                                                                                                                               Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 125020)
Holmes.S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 (4), 377-378 (2001)
                                                                                                                                                                                                                                   Direct Submission
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                                           /note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)" complement(35581. .35746)
complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                   /Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                            /map="16q24.3; between D16S520 and WI-12410"
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/protein_id="BAA20850.1"
/db_xref="GI:4433150"
                            _unit-ctg
                                                                                                                                                                                                                              Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
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934. .940
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Pred. No. 2.2e-15;
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                                                                                                                                                                51317 YKRWGKCTCRMWSWRKWRGCMGSAGGGSWRGAKYSMMSTSKYGSRWTCWMRSCWYWCTSC 51376
                                                                                                                                                                                                                                    51257 WWGMTTTWKYTKKTTTDVYKKKKSWKWKSKWTYTTCTKYTYYKTTKYTYWKTYTKGAGGW 51316
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                                                                                                                                                                                                554 tgcactcccatggtgatttctgcttggtctcctgctggggttggtggtactcgttcccac 613
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Local Similarity 12.4%; Pred. No. 0.0032;
hes 80; Conservative 293; Mismatches 269; Indels 5
 Sequence 14 from patent US 5670367.
I66494
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/db_xxef="01:17646245"
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NGAKKEGTWSNGLDDGYGTETYSDG"
NGAKKEGTWSNGLDDGYGTETYSDG"
NGAKKEGTWSNGLDDGYGTETYSDG"
29056 a 32731 c 30696 g 28283 t 4254 others
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/gene="JPH3"
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complement(<36507. .>36887)
/gene="JPH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             581 tctcctgctggggttggtggtactcgttcccaccgcacagaacccggcgcctattattgg 640
                                        source
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowloox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I66494.1 GI:2724471
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                                                                       Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                      Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Fifty-six TAC clopes which cover the 5.4 Mb Regions of the Genome
                                                                                                                                                                                                                                                                                                                                                                          Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                            29577 GACTTTATTCAGGTAAATAAGGTGATGCATGCCCCATTACATTTTCTTTTCTTTTCTCTC 29518
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29517 TGACCCCCTCTTCTCTTCTTCACTTGCATAGGTTCCTTTCACTGTATCTTTT 29464
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/note="TM0012b, a part of TAC clone:TM0012"
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WPI; 2001-514838/56
                                                     Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                         28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tggagggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tggagggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatcccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.5%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 7.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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AAI91235/c
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           Tang YT, Liu C,
                                         (HYSE-) HYSEQ INC.
                                                                                        28-FEB-2000;
                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                           18-MAY-2000;
                                                                                                                     26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                      WO200164835-A2
                                                                                                                                                                                                                     HOMO sapiens.
                                                                                                                                                                                                                                          nervous system disorders; arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 11295
                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             AAI91235
                                                                                                                                                                                                                                                                                                                                                                                                                      AAI91235 standard; cDNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, estimated the cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, insunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 428 BP; 203 A; 48 C; 92 G; 82 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctg 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 aagactgtaagtcgctgcctgagtggttttcatttttgtttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 tttttattgtcacacagaaaaggaaactgocttgtctccctttccgggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4183; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAO04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                                       2000US-0515126.
2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
          Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82; Indels
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AA182277/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAIT9941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to the encoded proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolynucleotides and polypeptides are useful in gene therapy, vaccines or polynucleotides and polypeptides have various cytokine-like activities, peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or activity and may be useful in the diagnosis and/or activity and may be useful in the diagnosis and treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 11295; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 415 BP; 185 A; 71 C; 91 G; 65 T; 3 other)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccggggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        AAI82277 standard; cDNA; 386 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; peptide therapy; stem cell growth factor; haemato
tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 2337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 ggttggtggtactcgttcccaccgcac 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctgg 591
                                                                                                                                                                                          nervous system disorders; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 CCTTGGGGGAATTTTTCTTCCCCCCCC
   28-FEB-2000;
18-MAY-2000;
                                                  26-FEB-2001; 2001WO-US04927.
                                                                                                                          WO200164835-A2
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
   2000US-0515126.
2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.5%;
51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 100; | Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 22; Length 415; pred. No. 0.0015;
                                                                                                                                                                                                                                       growth factor; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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AATB2334/C
ID AATB23
XX
AC AATB23
XX
AC AATB23
XX
O6-NOV
XX
Human

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or polynucleotides. The polypeptides have various cytokine-like activities, peptide therapy. The polypeptides have various cytokine-like activities, peptide therapy and factor activity, hammatopolesis regulating e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis and/or activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2337; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 386 BP; 213 A; 30 C; 52 G; 72 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iagnosing and treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI82334 standard; cDNA; 423 BP.
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                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI82334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 2394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctg 587
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                           26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                               WO200164835-A2
28-FEB-2000; 2000US-0515126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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 Mismatches

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RESULT 6
AA192484/c
ID AA1924
XX AA1924
XX AA1924
XX DT 06-NOV
XX Uman;
KW Vaccin
KW Vaccin
KW Vaccin
KW Vaccin
KW Vaccin
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KW Inervou
XX ING
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            WO200164835-A2
                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                             Homo sapiens.
                                                           nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                         Human polynucleotide SEQ ID NO 12544.
                                                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                               AAI92484 standard; cDNA; 442 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to Cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and tnflammation
                                                                                                                                                                                                                                                                                                                                               592 ggt 594
                                                                                                                                                                                                                                                                                                                                                          Sequence 423 BP; 205 A; 43 C; 87 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                   133 GTT 131
                                                                                                                                                                                                                                                                                                                                                                                      532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctgg 591
                                                                                                                                                                                                                                                                                                                                                                                                                                      472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2394; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AA002403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                      2001-514838/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45.4; DB 22; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Qγ
                                                                                                                                                                                                                            AAI85304/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                        Homo sapiens.
                                                                                                                 Human polynucleotide SEQ ID NO 5364.
                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                    AAI85304 standard; cDNA; 404 BP
                                                                                                                                                                                AA185304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                       199 TTTTTTTTTTTTTTTTTTTTT 177
                                                                                                                                                                                                                                                                                                 532 cttcttttgccctttcttagctt 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 442 BP; 175 A; 73 C; 104 G; 83 T; 7 other;
                                                                                                                                                                                                                                                                                                                      472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                             412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO000010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 12544; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAO12553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Drmanac RT
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.4; DB 22; Length 442; Pred. No. 0.0045;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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WO200164835-A2

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AAI83979/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human polynucleotides (AAi79941-AAi93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, this growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2000;
18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5364; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 404 BP; 205 A; 47 C; 82 G; 62 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                AAI83979 standard; cDNA; 416 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttt 471
              Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
                                                             Human polynucleotide SEQ ID NO 4039
                                                                                                                                                                                                                                                                                                                                                                                                           472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue growth factor; immunomodulatory; cancer;
                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                             532 cttcttttgccctttcttagcttgcactcccatggtgatttctqcttggtctcctgctgg 591
                                                                                                                                                                                                                                                                                                                                                                                592 ggttggtg 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                 70 AGATGGAG 63
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2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42.4; DB 22; Length 404; 
pred. No. 0.031; Indels 0
          leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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   WXX DEXX
                                                                                                                                                             AAI89184/c
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system disorders; arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200164835-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4039; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514838/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAOU4U48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 416 BP; 210 A; 44 C; 91 G; 66 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                               Human polynucleotide SEQ ID NO 9244.
                                                                                   06-NOV-2001 (first entry)
                                                                                                                                              AAI89184 standard; cDNA; 420 BP
                                                                                                                                                                                                                                                                                                                                                                         412 ttttttattgtcacacagaaaaggaaactgccttgtctccctttccgggaattctctcttt 471
Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
                                                                                                                                                                                                                                                                                        472 aagactgtaagtcgctgcctgagtggtttcattttgttttgttttcttcctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                      532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtct 583
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        51.7%;

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.6; DB pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                               83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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B X A X E
                                                                          AAS44777/c
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                                                                                                                                                                                                                Qγ
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                                                                                                                                                                                                                                                                                                       В
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                                 AAS44777;
                                                    AAS44777 standard; DNA; 424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, activity, tissue growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 420 BP; 204 A; 73 C; 65 G; 75 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                               223 TTTTTTTTTTATT 211
                                                                                                                                                        592 ggttggtggtact 604
                                                                                                                                                                          532 ottottttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctgg 591
                                                                                                                                                                                                                                  472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                       412 ttttttattgtcacacagaaaaggaaactgccttgtctccctttccgggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 9244; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                     5.7%;
Similarity 50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Drmanac RT,
(first entry)
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                Score 41.2; DB:
Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 420;
                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                                                  Indels
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as multiple sclerosis, connective tissue disease, rheumatoid arthritis, cdisorders such as Parkinson's disease, asthma and eczema, nervous system chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and cdisease, inflammatory disorders such as negative disease, Alzheimer's disease, Huntington's cdisease, ischaemia-reperfusion injury, shock, sepsis and inflammatory cell proliferation, cell differentiation, stem cell growth factor, cc activin or inhibin. Therefore, they can be used to manipulate stem cells augment or replace cells damaged by illness, accidental damage or genetic cartilage, tendons and ligaments and in tissue repair and bone, clored some sequences may also be used for regeneration, but were obtained in electronic format directly from wipo cat fip.wipo.int/pub/published_pct_sequences.
Sequence 424 BP; 138 A; 60 C; 110 G; 110 T; 6 other;
                                                                                                                                                                                                                                                                                                                               Sequences AAS44576-AAS44919 represent full-length polynucleotides and contig polynucleotides encoding polypeptides of the invention. The DNA and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as represented a such as leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 374; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-589862/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; neurous system disorder; inflammatory disorder; cell differentiation; ds; genetic disorder; bone regeneration; activin; inhibin; cartilage; burn; cytostatic; antinheumatic; antiarthritic; vulnerary; antinflammatory; neuroprotective; osteopathic; antidabetic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic; immunostimulant; analgesic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU27877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-2000;
14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human contig polynucleotide sequence #30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0515126.
2000US-0577409.
2000US-0597707.
2000US-0616807.
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Wehrman T, Wang J, Ma Y, Wang D, Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F;
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Query Match Best Local Similarity

5.7**%**; 57.6**%**;

Score 40.8; DB Pred. No. 0.093;

DB 22; Length 424;

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AAI81389/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 1449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI81389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI81389 standard; cDNA; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 ttttattgtcacacagaaaaggaaactgccttgtctcccttccggggaattctctctttaa 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer lenvesments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 TTTTT 217
                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1449; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAO01458
                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                              treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tcttt 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gactgraagtcgctgcctgagtggtttcattttgtttttgtttttctgcccttctctttct 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Query Match

sequence 400 BP; 184 A; 50 C; 85 G; 80 T; 1 other;

5.6%;

Score 40.6;

DB 22;

Length 400;

Sequence 410 BP; 197 A; 36 C; 119 G; 50 T; 8 other;

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RESULT 12
AAI89131/c
ID AAI891
Best Local Similarity 52.7 Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 9191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI89131 standard; cDNA; 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nervous system disorders; arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctctt 531
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927.
                                                                                                                         production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, peptide therapy. The polypeptides have various cytokine-like activities are seen cell growth factor activity, haematopoiesis regulating activity and activity, tissue growth factor activity, immunomodulatory activity and activity, indicatory activity and may be useful in the diagnosis and/or activity in the diagnosis and/or activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 9191; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-514838/56.
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RESULT 13
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                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer landrammia narrowne greatem diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                  treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                          Claim 1; SEQ ID NO 12539; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 12539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI92479;
               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cttcttttgccctttcttagctt 554
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                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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55.2%;

 Mismatches

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Sequence 410 BP; 170 A; 54 C; 107 G; 71 T; 8 other;

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AAZ17263/c
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12332 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the differentially expressed genes correlated with the differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides
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                                                                                                                                                                             Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1998;
28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                        Novel human genes and their expression products of differentially expressed in different cell types
                                                                                                                                                                                                                                                        WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                   Stache-Crain B,
                                                                                                                                                                                                                                                                                            Jones WL, Kassam A, Ke
Lamson G, Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                          Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                            Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09938972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene expression product cDNA sequence SEQ ID NO:4735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 ttttttattgtcacacagaaaaggaaactgccttgtctccctttccggggaattctctcttt 471
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                                                                                                                                                                                                                                                                                                                       Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                 Dickson M, Drmanac R, arcia PD, Garcia V, Giese K, Innis Jsam A, Kennedy GC, Kita D, Labat I; hkowitz D, Pot D, Randazzo F, Reinb Jahrh-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                          98US-0080515
                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0075954
98US-0080114
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0072910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980S-0080666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US01619
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                                                                                                                                                                                                                         products which are
                                                                                                                                                                                                                                                                                                                    Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Indels
                                                                                                                                                                                                                                                                                           Reinhard C;
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RESULT 15
AA188050/c
ID AA1880
AC AA1880
AC AA1880
AC Human
XX Human
XX Human
XX Human
KW Vaccin
KW Vaccin
KW O7-SE
XX Homo S
YX 28-FE
PR 18-MA
XX HTSE
PR 18-MA
XX HYSE
PR 18-MA
XX ISOld
PR PPSI
XX ISOld
PR ISO
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The polynucleotides may also be used to construct therapeutic for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify a genetic predisposition or susceptibility to a disease such as identify as identified as
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18-MAY-2000; 2000US-0577409.
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             Claim 1; SEQ ID NO 8110; 1399pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification.
                                                                                                                                                                                                                               e.g. stem cell growth factor activity, haemaropoies, a require restrictly and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or activin/inhibin activity and may be useful in the diagnosis and/or activin/inhibin activity and may be useful in the diagnosis anthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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Sequence 398 BP; 162 A; 72 C; 71 G; 81 T; 12 other;

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US-08-132-809-1
US-08-520-678A-24
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-14 -Application US/0823246 5670367 FORMATION: T: PORNER, F. T: SCHIFILINGER, F. T: SCHIFILINGER, F. T: PALKNER, F. TINGES: SEE: Foley & Lardner SEE: Foley & Lardner SEE: Foley & Lardner SEE: Foley & Lardner SEE: FORM: Alexandria VA TYPE: Floppy disk A TYPE: Floppy disk A TYPE: Floppy disk A TYPE: FLOPPY TING SYSTEM: PC-DOS/MS- ARELICATION NUMBER: US/08/23 APPLICATION NUMBER: US/08/23 G DATE: CATION NUMBER: US/07/93 G DATE: CATION NUMBER: EP 91 11 G DATE: 26-AUG-1991 Y/AGENT INFORMATION: BENT, Stephen A SENCE/OCKET NUMBER: 300 MUNICATION INFORMATION: BENT, STEPHER 1093 SINGLE/OCKET NUMBER: 300 MUNICATION INFORMATICS: ECHARACTERISTICS: ECHARACTERISTICS: HONE SEG ID NO: 14: SEGUE/OSY: Linear TYE SOURCE: ET PTZ9T-F1S S3-14	1635 5433 20303 26764 1431 1431 1798 13613 313613 313613 7208 7208 1065 1065 1065 1065 1065
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ion US/08232463  ion US/08232463  R, F. G. R, F. G. R, F. G. RE, G. RE, F. G	US-09-234-332-4 US-08-929-329-1 US-08-370-975B-6 US-08-370-975B-1 US-09-018-584A-8 US-09-018-584A-8 US-09-105-537-21 US-08-557-128-12 US-09-105-537-3 US-09-105-537-3 US-09-329-796-1 US-09-313-932-107
	sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 21, Appli Sequence 21, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 107, App Sequence 107, App Sequence 1, Appli Sequence 1, Appli

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INFORMATION FOR SEQ ID NO: 14:
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Best Local :
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IMMEDIATE SOURCE:
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                         NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                           FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 ccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccag 692
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 attetetetttaagaetgtaagtegetgeetgagtggttteattttgtttttgtttttetg 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
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                                                                   nucleic acid
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                                                     single
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26-AUG-1991
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US-08-162-809-1
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Best Local Similarity
""+"hes 8; Conserve
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Patent No. 5457048
GENERAL INFORMATION:
                                                                                                             TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                  FEATURE:
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3133 base pairs
                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pasquale,
APPLICANT: Sajjadi,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                              MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
    NAME/KEY:
LOCATION:
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                                                                         TYPE:
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                                                          STRANDEDNESS:
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                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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CITY: San Diego
STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasquale, Elena B.
Sajjadi, Fereydoun G.
Sajjadi, Fereydoun G.
WENTION: NOVEL EPH-RELATED TYROSINE KINASES,
WYENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
join(3..419, 421..2858)
                CDS
                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                            linear
                                                                                                                                           (619)
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                                                          both
                                                                                                                             535-8949
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US-08-162-809-1

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Best Local Similarity 48.6%;
Matches 105; Conservative
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                                     Matches
                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3004 GGGACTCGCCTCGGCCTGGTGACTTCCATCCCTCAC 3039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2884 GACGGGGAGGCAGGTGGCAGAGGTGGGAGGGAGCAACTGATCTGATGGGAGCCGTGGG 2943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: Howell & Haferkamp, L.C.
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2944 GCCGCAGCTGGAGAGGGGCAGCCACGGCCGGGGGCTGTGCCTGACCGCGGAGGACGTTCCT 3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 accccggttggagagaggagcggaactcctggacaagccctgacaagccaagccaaaggt 189
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
                                                                                                                                                                                                                                                                                                      TELEPHONE: 314-727-5188
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STREET:
CITY: S
                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                    NAME: Henderson, Melodie W. REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/520,678A
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                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                   TELEFAX:
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                                                     Local Similarity
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                                                                                                                                           DNA (genomic)
                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                         6029-6836
                                                       Score 37.8;
Pred. No. 0.
                                        Mismatches
                                                       0.083;
                                                                      DB 2; | Length 257;
                                        47; Indels
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US-08-897-126-24
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US-09-268-992-7/c

; Sequence 7, Application US/09268992

; Patent No. 6342351
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                                                  RESULT
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Sequence 24, App
Sequence 24, App
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Best Local :
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                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rice, Charles M.
APPLICANT: KOLYKhalov, Alexander A.
APPLICANT: KOLYKhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 TTTTTTTTCTTTCCTTCCTTTTTCCCTTTCTTTCTTCCTTCTTTAATGGTGG 226
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                     174 TTTTTTTTCTTTCCTTCCTTTTTCCCTTTCTTTCTTCCTTCTTTAATGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Henderson, Melodie W. REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                         Local Similarity
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7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice, Charles M.
                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                           5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/520,678
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                           Score 37.8; DB 4; Length 257; Pred. No. 0.083;
                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                              Gaps
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GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 123
                                                                                                                        ; OTHER INFORMATION: Translation template US-09-007-005-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-007-005-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: n=a, c, g, or t US-09-268-992-7
               Matches
                                    Best. Local
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09007005B Patent No. 6258558
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00706/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Szostak, Jack w. APPLICANT: Roberts, Richard w. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
LENGTH: 72604
                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER FILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 60/078,044
                                                                                                                                                                                                           TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, H.
APPLICANT: Freimer, N.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
LOCATION: all n positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 tgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgct 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 5.2%; Local Similarity 58.6%;
         on 5.2%; Score 37.2; DB 4; Length 123; I Similarity 39.1%; Pred. No. 0.091; One 123; Similarity 29; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65;
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  29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mismatches
      27;
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    Indels
    0;
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Gaps
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0;
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APPLICANT: SZOSTEK, Jack W.

APPLICANT: Liu, Rihe
APPLICANT: Liu, Rihe
ITILE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
ITILE OF INVENTION: FUSIONS
IFILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-01-27
LEARLIER FILING DATE: 1998-01-14
NUMBER OF SEO ID NOS: 33
COPTWARRE FEASTERD FOR WINDOWS VARSION 4 0
; NAME/KEY: CDS
; LOCATION: (212)..(3988)
US-09-339-964-1
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                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09339964 Patent No. 6025198 GENERAL INFORMATION:
                                                                                                                      SEQ ID NO 1
LENGTH: 4743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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LENGTH: 123
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                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/339,964
CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                         APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
FILE REFERENCE: RTS-0065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                               NUMBER OF SEQ ID NOS: 47
                                                                           ORGANISM: Homo sapiens
                                                              FEATURE:
                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 TITTTTTTTTTTTTTTTTTTTGYTYTYCYAYGYGYTYCYTYTYCYTYTYCYAYGYAYGYA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558 ctcccatggtgatttctgcttggtctcctgct 589
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NAME/KEY: misc_feature

; LOCATION: (1)...(152331)

; OTHER INFORMATION: n = A,T,C or G

US-09-128-155-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL MOLECULES TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pan, Yang
                                                                                                            Sequence 13, Application US/09018584A Patent No. 6238863
GENERAL INFORMATION:
APPLICANT: Schumm, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
TITLE OF INVENTION: REPEAT DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4348 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccaccccccgctggg 4407
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                   125 gggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaagcca 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 tgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ccgctgggcaggcgggcagctccgggcgctcctcggagaccactgcgctccacgttgagg 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 152331;
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US-09-018-584A-13
                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-659-251-14/c
                                                                                                                                                                                                                                                        ; Patent No. 5883081 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: G132
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 257-3501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                              APPLICANT: Talbott, Rainer
APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                     APPLICANT: Kraus, Guenter
APPLICANT: Wong-Staal, Fl
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                549 tagcttgcactcccatggtgatttctgcttggtctcctgct 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 cctgagtggtttcattttgttttgtttttctgcccttctctttttcttttttctttttgccctttct 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Watch 4.9%; score 35.4; DB 4; Length 372; Local Similarity 59.4%; pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                           94 TTTCTTTTCCTTTCCTTTTCTTCTTCTCTCTCTCTCT 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                COUNTRY: USA
ZIP: 94111-3834
                                                                                    CITY: San Francisco
                                                                                                 STREET:
                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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G132
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                                                                                                  E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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Talbott, Randy
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                                                                                                                                                                                                                                        Patent No. 6235881
GENERAL INFORMATION:
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                                     APPLICANT: Talbott, Kanuy
APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 02307E-(TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                             128 GGAC 125
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OTHER INFORMATION:
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PRIOR APPLICATION DATA:
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                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3168 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/001,441 FILING DATE: 26-JUL-1995
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                   94111-3834
                                    USA
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Talbott, Randy
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SYSTEM: PC-DOS/MS-DOS
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49.5%; Pred. No. 1.3;
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/note= "HIV-2KR subsequence encoding
pol gene"
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COMPUTER: FLORE FORM:
MEDIUM TYPE: Florey disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
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LOCATION: 1..3168
LOCATION: 0..3168
OTHER INFORMATION:
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                                                                                                                                 STREET: 201 N. Figueroa Street, 5th Floor CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                          555 gcactcccatggtgatttctgcttggtctcctgctgggggttggtggtactcgttcccacc 614
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APPLICATION NUMBER:
                                                                                               COUNTRY:
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                                                                                                                 STATE:
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Local Similarity 49.5%;
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STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
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COMPUTER: II
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                                                                                90012-2628
                                                                                                               California
                                                                                                                                                                                                                The Regents of the University of California VENTION: Isolation of Novel HIV-2 Proviruse:
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/note= "HIV-2KR subsequence encoding
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Pred. No. 1.
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TELEPHONE: (213) 977-1001
TELEPHONE: (213) 977-1003
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                            APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
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                                                                                                           ZIP: 94111-3834
                                                                                                                       COUNTRY:
                                                                                                                                                           CITY: San Francisco
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49.5%; Pred. No. 1.3;
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/note= "HIV-2KR subsequence encoding
pol gene"
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Search completed: September Job time: 28877 sec

7, 2002, 18:23:03

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10163 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                  Query Match 4.9%;
Best Local Similarity 49.5%;
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,441
FILING DATE: 26-JUL-1995
ATTORNBY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                2601 GCAAATCCTCTGTCGCCTCTTTGTGTGGTGTCTCTCCTTGTTCGAGGTGCAGTAAGTCCT 2542
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                               2481 ACTTCTCTAGCAGGTCTGCTGGGGGTCTGCTGGGGGGTGCTGTTGGTGTCAGCCCCTGCG 2422
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                               2541 CTGTCACCTTCTATGGTCTCATTTTCTGCTCTTTCTGCTTCCTCCTTGCTGCAAGT 2482
2421 GGAC 2418
                               615 gcac 618
                                                                                   555 gcactcccatggtgatttctgcttggtctccctgctggtggtttggtggtactcgttcccacc 614
                                                                                                                                                             435 gaaactgccttgtctcccttccgggaattctctcttttaagactgtaagtcgctgcctgag 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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514
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                                                                                                                                                                                                                                                                                       Score 35.2;
Pred. No. 2;
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Gaps

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 10
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1: /cgn2_6/ptcdata/2/pna/US06_COMB.seq:*

2: /cgn2_6/ptcdata/2/pna/US07_COMB.seq:*

3: /cgn2_6/ptcdata/2/pna/US07_COMB.seq:*

4: /cgn2_6/ptcdata/2/pna/US08_COMB.seq:*

4: /cgn2_6/ptcdata/2/pna/US08_COMB.seq:*

5: /cgn2_6/ptcdata/2/pna/US083_COMB.seq:*

7: /cgn2_6/ptcdata/2/pna/US083_COMB.seq:*

8: /cgn2_6/ptcdata/2/pna/US085_COMB.seq:*

9: /cgn2_6/ptcdata/2/pna/US085_COMB.seq:*

10: /cgn2_6/ptcdata/2/pna/US085_COMB.seq:*

11: /cgn2_6/ptcdata/2/pna/US086_COMB.seq:*

12: /cgn2_6/ptcdata/2/pna/US089_COMB.seq:*

13: /cgn2_6/ptcdata/2/pna/US089_COMB.seq:*

14: /cgn2_6/ptcdata/2/pna/US089_COMB.seq:*

15: /cgn2_6/ptcdata/2/pna/US089_COMB.seq:*

16: /cgn2_6/ptcdata/2/pna/US091_COMB.seq:*

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18: /cgn2_6/ptcdata/2/pna/US091_COMB.seq:*

19: /cgn2_6/ptcdata/2/pna/US091_COMB.seq:*

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10: /cgn2_6/ptcdata/2/pna/US091_COMB.seq:*
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Listing first 45 summaries
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cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US009C_COMB.seq:*
/cgn2_6/ptodata/2/pna/US009C_COMB.seq:*
/cgn2_6/ptodata/2/pna/US000C_COMB.seq:*
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44: /cgn2_6/ptodata/2/pna/US6005_COMB.seq: * 45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq: * 46: /cgn2_6/ptodata/2/pna/US6006_COMB.seq: * 47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq: * 49: /cgn2_6/ptodata/2/pna/US6008_COMB.seq: * 49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq: * 50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 51: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 52: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 53: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 55: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 56: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 57: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 59: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 59: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 59: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 59: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: * 60: /cgn2_6/ptodata/2/pna/US6010_COMB.seq: * 61: /cgn2_6/ptodata/2/pna/US6010_COMB.seq: * 62: /cgn2_6/ptodata/2/pna/US6010_COMB.seq: * 63: /cgn2_6/ptodata/2/pna/US6010_COMB.seq: * 64: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 66: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 66: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 67: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 67: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 67: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 70: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 70: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: * 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq: * 71: /cgn2_6/ptodata/2/pna/US6031_COMB.seq: * 73: /cgn2_6/ptodata/2/pna/US6035_COMB.seq: * 73: /cgn2_6/ptodata/2/pna/US6036_COMB.seq: * 73: /cgn2_6/ptodata/2/pna/US6036_COMB.seq: * 73: /cgn2_6/ptodata/2
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		Sequence 581, App	8889,	16/2,	7000		0 F C F C	D	9888,	3862,	4710,	Sequence 23549,	1341,	Sequence 39624,	6 26/2	Sequence 39524	Sequence 38/9/		04/	,8560 9	e 2214,	727	331	8 T B		32,	3/05	4	. u	· -	, F	N د	!	Description

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Sequence 2, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
PLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-2
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PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                  1 gatcccgctgggcaggcggggcagctcctcgggcgctcctcggagaccactgcgctccaccgtt 60
                           ctcgaaaaagttatatgggggctgaatgagcttctggaggcttgtttaccgttttttatt
                                                                  gagcctacagccttcagaacacatattgctcattttctggcagttctcagacgtaggaaa
                                                                             gagcctacagccttcagaacacatattgctcattttctggcagttctcagacgtaggaaa
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                                                                                                                                                                                                                                                                    Conservative
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US-09-362-510A-3927

US-09-904-013-3927

US-60-172-373-10224

US-09-652-127-2780

US-09-652-127-2780

US-09-652-111-10283

US-09-652-911-10283

US-09-365-615B-94

US-09-802-669-94

US-09-431-517-12091

US-09-431-517-12154
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12154, A
24990, A
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3927, Ap
10224, Ap
10224, Ap
2780, Ap
2780, Ap
10283, Ap
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; Sequence 10, Applica
; GENERAL INFORMATION:
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LENGTH: 45121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
10794 taagtcagcaccgaagcagtggttaagccggagggctcggaagaacggcaccttttcttt
                                                                                                                                                      10674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                    301 taagtcagcagcagagcagtggttaagccggagggctcggaagaacggcaccttttcttt 360
                                                                                        241 gagcetacageetteagaacacatattgeteattttetggeagtteteagaegtaggaaa
                                                                                                                                                                                                                                  121 tggagggggaccccggttggagaggagggggaactcctggacaagccctgacaagccaa
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                                                                         gagcctgcagccttcagaacagatattgctcattttctggcagttctcagacgtaggaaa 10793
                                                                                                                                          gaggtgggcgtgggggggacaggaattgaagcggaagtctgggaagctttagggtcgc
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Pred No. 3.2e-151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
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CURRENT EILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE9/03343
PRIOR FILLING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILLING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Krammer, Peter APPLICANT: Muller-Schill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
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                                                                                     gccaaaggtccgctccggcgcgggtgggtgagtgcgccccgcccccgcggggggcggggaga 240
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                                                                   gccaaaggtccgctccggcgcgggtgggtgagtgcgcgccgccgccccccgcggggggcggggaga
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                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                          99.0%; Score 713; DB 32; 100.0%; Pred. No. 1.3e-150;
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                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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661 gttttgaaaagtccctcgctcagaaatgccagcttgcagatggctaatcaaag 713
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99.7%;
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Pred. No. 8.8e-128;
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GENERAL INFORMATION:

APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Ozen, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
VOMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 2827
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                 286 ctcagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa 345
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                                                                               909999909999agagagoctacagocttcagaacacatattgotcattttctggcagtt 285
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; OTHER INFORMATION: Incyte ID No: 038693.2c
US-60-172-360-3705
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APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
FILE REFERENCE: GX-0007 p
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOTWARE: PERL Program
SEQ ID NO 3705
LENGTH: 467
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                        287 TACTCGTTCTCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT
              601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct
                                                                              541 ccctttcttagcttgcactcccatggtgatttctgcttggtctcctctgctggggttggtgg
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99.3%;
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Pred. No. 9.1e-57;
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; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-32
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-489-036-818
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
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Best Local Similarity
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PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                    CURRENT APPLICATION NUMBER: US/09/489,036
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 818
LENGTH: 419
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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                                                                                                                                                                                  TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries
                                                                                                                                                                FILE REFERENCE: 783
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Pred. No. 3.9e-49;
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PRIOR APPLICATION NUMBER: 09/489,036
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 818
LENGTH: 419
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-143-818
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; Sequence 3315, Application US/09471275; GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained; TITLE OF INVENTION: From Various Libraries; FILE REFERENCE: 782
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CURRENT FILING DATE: 2001-08-30
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TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 gaccccgctgggcaggcgggcagctcctgggcgctcctcggagaccactgcgctccacgtt 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 gccaaaggtccgctccggcgcgggt 205
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                                                                                                                                                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                                                                                                                                                                                                                                             181 gccaaaggtccgctccggcgcgggt 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaggtgggcgtggggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 203.4; DB 35; Length 419; Pred. No. 1.1e-35;
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CURRENT APPLICATION NUMBER: US/09/471,275

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RESULT 11
US-09-333-909-2214
; Sequence 2214, Application US/09333909
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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** NAME/KEY: misc_feature
** LOCATION: (465)...(578)
** OTHER INFORMATION: similar to gi178067 in the genepept database release 114,
** OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-471-275-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: pt_C
SEQ ID NO 3315
LENGTH: 575
           APPLICANT: Gearing, David P.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED
TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY
FILE REFERENCE: MLN98-29pM
CURRENT APPLICATION NUMBER: US/09/333,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 204;
CURRENT FILING DATE: 1999-06-16
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EARLIER
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EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
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EARLIER FILING DATE: 1999-03-25
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                                                                                                                                                                                                                                                                                                  181 gccaaaggtccgctccggcgcgggt 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                         253 GAGGTGGGCGTGGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 GACCCCGCTGGGCAGGCGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 254
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                                                                                                                                                                                                                                                                                                                                                          TGGAGGGGGACCCCGGTTGGAGAGAGGGGGGGAACTCCTGGACAAGCCCTGACAAGCCCAA
                                                                                                                                                                                                                                                                            GCCAAAGGTCCGCTCCGGCGCGGGT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/126,605
FILING DATE: 1999-03-26
APPLICATION NUMBER: US 09/306,350
FILING DATE: 1999-05-07
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APPLICATION NUMBER: US 60/125,453
FILING DATE: 1999-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/293,972 FILING DATE: 1999-04-15 APPLICATION NUMBER: US 09/274,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/271,490 FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/240,371 FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/234,611
FILING DATE: 1999-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-12-23
APPLICATION NUMBER: US 09/235,076
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; TYPE: DNA; OTHER SAPIENS; ORACHISM: Homo sapiens; FEATUREM; Misc_feature; LOCATION: (1)...(466); OTHER INFORMATION: n = A,T,C or GUS-09-817-500-2214
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/817,500
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/089,519
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/135,628
PRIOR APPLICATION NUMBER: US 60/135,628
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-06-16
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 2409
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US-09-817-500-2214
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                                         Query Match
Best Local
                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2214
LENGTH: 466
                     Matches
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EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1999-05-24
RUMBER OF SEQ ID NOS: 2409
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY FILE REFERENCE: 1600.1029-002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gearing, David P. APPLICANT: Pan, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(466)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
Local 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 ctttaagactgttcttacgtctgttgctagattatcgtccaaaagtgttaatgccc 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 otttaagactgtaagtcgctgagtggtttcattttgtttttgtttttctgccc 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 cagacgtaggaaataagtcagcagcagcagtggttaagccggagggctcggaagaacg 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accgttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctct 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcaccttttctttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgttt 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcaccttttcttctcgaaaaagttatatgggggctgaatgagcttcttggaggcttgttt 407
                                       Similarity
                 Conservative
                                  26.4%;
87.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.4%;
87.7%;
        Score 190.2; DB 31; Length 466; Pred. No. 1.1e-32; 0; Mismatches 29; Indels 0;
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             0;
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        Gaps
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          0;
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288 cagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaacg 347

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GENERAL INFORMATION:
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5938
LENGTH: 532
                                                                         GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: HOLTZMAN, DOUGLAS A.
APPLICANT: HOLTZMAN, DOUGLAS A.
APPLICANT: HOLTZMAN, DOUGLAS A.
APPLICANTION: NUCLEIC ACID MOLECULES DERIVED, FI
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
FILE REFERENCE: 1600.1086-001
CURRENT APPLICATION NUMBER: US/09/522,303
CURRENT FILING DATE: 2000-03-08
CURRENT FILING DATE: 2000-03-08
CURRENT FILING DATE: 2000-03-08
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Best Local Similarity
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2051-001
CURRENT APPLICATION NUMBER: US/09/726,788
CURRENT FILING DATE: 2000-11-30
CURRENT FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gearing, David P. APPLICANT: Kingsbury, Gilli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/168,131 PRIOR FILING DATE: 1999-11-30
EARLIER APPLICATION NUMBER: 60/123,393
EARLIER FILLING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                              466 ctctttaagactgtaagtcgctgcctgagtggtttcattttgtttttgtttttcttgccc 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 cccgcacgtcggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggcaccttttctttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgt 405
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    Mismatches

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PRIOR APPLICATION NUMBER: 60/14:
PRIOR FILLING DATE: 1999-07-14
NUMBER OF SEQ ID NOS: 2240
SOFTWARE: FastSEQ for Windows V.
SEQ ID NO 898
LENGTH: 362
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Best Local Similarity
Matches 193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HOITZMAN, DUNY---
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
TITLE REFERENCE: 1600.1146-001
PTIE REFERENCE: 1600.1146-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                              Query Match
Best Local :
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CURRENT FILING DATE: 2000-07-14
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 ctccggcgcgggtgggttcttacg 256
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               193 ctccggcgcgggtgggtgagtgcg 216
                                                                                133 coggttggagagagagagagagactcctggacaagccctgacaagccaaagccaaaggtccg
                                                                                                                              113 gggtgcggacaggaattgaagcggaagtctgggaagctttagggtcgctggagggggacc
                                                                                                                                                                                            53 cggcggggcacgctccggcgctcctcggagaccactgcgctccacgttgaggtgggcgtg 112
                                                                                                                                                                                                             13 caggcggggcagctcccggcgctcctcggagaccactgcgctccacgttgaggtgggcgtg 72
                                                                                                                                                                                                                                                                            Local Similarity
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                                                           ccggttggagagaggggaactcctggacaagccctgacaagccaagccaaaggtccg
                                                                                                                                            99999c99acaq9aattgaaqcg9aagtcttg9gaagctttag99tc9ctg9ag9999gacc 132
ctccggcgcgggtgggttcttacg
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94.6%;
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Pred. No. 7.5e-32;
                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                Score 186.4; DB 2
Pred. No. 7.5e-32;
   256
                                                                                                                                                                                                                                                                                                 DB 23;
                                                                                                                                                                                                                                                                    11; Indels
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Search completed: September 7, 2002, 22:32:03 Job time: 43817 sec

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
            Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/P

2: /cgn2_6/ptodata/2/pna/U

3: /cgn2_6/ptodata/2/pna/U

4: /cgn2_6/ptodata/2/pna/U

5: /cgn2_6/ptodata/2/pna/U

5: /cgn2_6/ptodata/2/pna/U

6: /cgn2_6/ptodata/2/pna/U

8: /cgn2_6/ptodata/2/pna/U
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                            : /cgn2_6/ptodata/2/pna/PCT_NEW_COMB: seq:*
/cgn2_6/ptodata/2/pna/US06_NEW_COMB: seq:*
: /cgn2_6/ptodata/2/pna/US08_NEW_COMB: seq:*
: /cgn2_6/ptodata/2/pna/US08_NEW_COMB: seq:*
: /cgn2_6/ptodata/2/pna/US09_NEW_COMB: seq:*
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US-10-035-832-1262
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US-10-098-754-7588
US-10-155-881-6250
US-10-155-881-6297
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US-10-176-912-202
US-10-184-634-202
US-10-184-634-202
US-10-035-832-39388
US-10-035-832-39388
US-10-035-832-39388
                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
 Sequence 1262, Ap
Sequence 8585, Ap
Sequence 8585, Ap
Sequence 7588, Ap
Sequence 2987, Ap
Sequence 114395,
Sequence 114395,
Sequence 114395,
Sequence 117396,
Sequence 532, App
Sequence 561, App
Sequence 971, App
Sequence 971, App
Sequence 971, App
Sequence 272, Appl
Sequence 272, Appl
Sequence 202, Appl
Sequence 33988, Appl
Sequence 6470, Appl
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1061 18 1067 24 1073	Query   Best L Matche 1 1049 1 1055	ULT 10-035 EQUENCE EQUENCE APPLIC APPLIC TILE I FILE I CURRED CURRED PRIOR PRI		2226 2227 2227 2322 2322 2322 2323 2324 2424 24
4 tggag 1 gccaa             4 gccaa             4 gccaa 1 gagcc 1 gagcc 1 taagt	Match Local Simi Local Simi S 718; 1 gatcocy 1 gatcocy 1 gaggtgy 1 gaggtgy 1 gaggtgy 1 gaggtgy	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		38.2 38.2 38.2 3.2 3.2 3.3 3.3 3.3 3.3 3.3 3
gggacccg gggacccg ggtcgctc           acagccttc           cagcaccgaa	larity Conserv ctgggca          ctgggca gcgtggg gcgtggg	SEGULT 1 Sequence 1262, Application US/ GENERAL INFORMATION: APPLICANT: MORTIS, David APPLICANT: Engelhard, Eric APPLICANT: Engelhard, Eric APPLICANT: Engelhard, Eric APPLICANT: Engelhard, Eric CURRENT APPLICATION NUMBER: US PRIOR FILING DATE: 2002-07 PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2010-03-03 NUMBER OF SEQ ID NOS: 1613 SOFTWARE: Patentin version 3. SEQ ID NO 1262 LENGTH: 45121 TYPE: DNA ORGANISM: Homo sapiens		5.3 148 5.3 148 5.3 148 5.3 79 5.2 11895 5.2 11895 5.2 12404 5.2 12404 5.2 655 5.2 655 5.2 655 5.2 655 5.2 655 5.2 655 5.2 655 5.2 655 5.2 655 5.2 70 5.2 70 5.2 70
ttgg ttgg               gaac 	99.6 199.7 199.7 1999 1999 19099 1111	on US  d  d  CEL CO  FRMS  002-0  002-0  003-0  003-0  003-0  003-0  003-0  003-0  003-0  003-0  003-0		5677757755
gaggagcggaactcctggacaagg gaggagcggaactccttgaccagg griggttgagtgcgcgcccgc 	; Score 716.8; DB 6; Le ; pred. No. 3.1e-165; 0; Mismatches 2; In cagctcoggcgctcctcggagaccac [	,/10035832  MPOSITIONS AND METHODS FOR US/10/035,832 17-22 19-727,377 12 109/798,586 109/798,586	ALIGNMENTS	US-09-918-995-18465 US-10-155-881-3906 US-10-155-881-3250 US-10-155-881-2250 US-10-027-632-163595 US-10-027-632-133145 US-10-158-314-24 PCT-US02-17313-11 US-10-161-572-11 US-10-027-632-229380 US-10-027-632-229381 US-10-027-632-229381 US-10-027-632-229381 US-10-027-632-229381 US-10-027-632-229381 US-10-027-632-10-058-544-10705 US-10-027-632-10-058-544-10705 US-10-011-154-4558 US-10-027-632-10-3277 US-10-098-754-6901 US-09-691-064-7
cctgacaagca cctgacaagca gggggcgggag                cagacgtaggaa              cagacgtaggaa cagacgttttctt	ngth 45121;  dels 0; Gaps  tgcgctccacgtt 60  [             tgcgctccacgtt 10553  tgcgtttagggtcgc 120                  gcttttagggtcgc 10613	CANCER		Sequence 18465, A Sequence 3906, Ap Sequence 2250, Ap Sequence 163959, Sequence 163959, Sequence 113345, Sequence 11, Appl Sequence 11, Appl Sequence 1288, Ap Sequence 229379, Sequence 229380, Sequence 229380, Sequence 229380, Sequence 239381, Sequence 239381, Sequence 10705, Ap Sequence 10705, Apsequence 103277, Sequence 103277, Sequence 103277, Sequence 6901, Ap

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APPLICANT: Rosen et al.
TIFLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM006C1N
CURRENT APPLICATION NUMBER: US/10/222,927
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/758,465
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1276
CORTWARE PATENTIN VET 2.0
                                                    RESULT 3
US-10-198-846-8585
; Sequence 8585, Application US/10198846
; GENERAL INFORMATION:
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SEQ ID NO 123
LENGTH: 710
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local
   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 123, Application US/10222927 GENERAL INFORMATION:
                                APPLICANT: Lillie, James APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11154 gttttgaaaagtccctcgctcagaaatgccagcttgcagatggctaatcaaagagacgtg 11213
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                                                                                                                                                                       529 tttcttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctc 584
                                                                                                                                                                                                                     661 gttttgamaagtccctcgctcagaaatgccagcttgcagatggctaatcaaagagacgtg 720
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Steinmann, Kathleen
             Xu, Yongyao
Wang, Youzhen
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; Sequence 7588, Application US/10098754; GENERAL INFORMATION:
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CURRENT EPILICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FAST-SEQ for Windows Version 4.0

LENGTH: 931

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LOCATION: 541, 542, 544, 550, 554, 555, 557, 561,
LOCATION: 607, 629, 638, 658, 660, 663, 666, 675,
LOCATION: 718, 724, 726, 728, 732, 735, 746, 749,
LOCATION: 770, 773, 779, 780, 792, 800, 801, 822,
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LOCATION: 229, 231, 234, 256, 294, 295, 299, 309,
LOCATION: 339, 344, 357, 360, 361, 363, 366, 369,
LOCATION: 412, 418, 424, 426, 428, 432, 437, 441,
LOCATION: 462, 463, 470, 471, 472, 478, 503, 506,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 832, 833, 843, 845, 854,
LOCATION: 909, 929, 930
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gttgaggtgggcgtggggcggacaggaattgaagcggaagtctgggaagctttagggt 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 101; Indels
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380,
444,
520,
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, 387, 397, 407,
, 456, 459, 460,
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APPLICANT:
APPLICANT:

APPLICANT:

Sherf, Bruce Cain, Scott Rundlett, St

Bruce A. Stephen

APPLICANT: Harrington, John J. APPLICANT: Jackson, P. David

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; NAME/KEY: misc_feature
. LCCATION: (1)...(1021)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-7588
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              S
                                                                                                                                     ; ORGANISM: Zea mays
US-10-155-881-6250
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.7%;
Best Local Similarity 52.3%;
Matches 90; Conservative
                                                                                                                                                                                    SEQ ID NO 6250
LENGTH: 2319
                                                                                                                                                                                                                                APPLICANT: Liu, Jingdong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/791539
PRIOR FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dotson, Stanton APPLICANT: Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 37595
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                                                                                                                                                                     TYPE: DNA
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Local Similarity 47.2%;
hes 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40.8; DB 6; Length 1
Pred. No. 3.2;
0; Mismatches 131; Indels
                                                     0; Mismatches
                                                                     Score 40.8; DB 7; pred. No. 3.9;
                                                   82; | Indels
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                                                                                     Length 2319;
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                                                       Gaps
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; TYPE: DNA
; ORGANISM: Zea mays
US-10-155-881-2987
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                                                                                                                                     Sequence 104181, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
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SEQ ID NO 2987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: TRANSCRIPTION IN PLANTS FILE REFERENCE: 38-21(15300)J CURRENT APPLICATION NUMBER: US/10/155,881 CURRENT FILING DATE: 2002-05-22
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APPLICANT:
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               CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1200 TTTTTTTTTTTTTTTTTACACAGAACAGATACAAATACATAGACAAGCAAAGCAACTA 1141
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                                                                                                                                                                                                                                                                                                                                                                                            652 gagcagcctgttt 664
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McIninch, James
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47.4%; Pred. No. 5.1;
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; ORGANISM: Human
US-10-027-632-174395
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILLING DATE: 2000-07-12
PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 174395
LENGTH: 787
                                                                                              Query Match
                                                       Matches
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Best Local Similarity 55.6%;
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LENGTH: 787
TYPE: DNA
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTEED for Windows Version 4.0
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
424 acacagaaaaggaaactgccttgtctccctttccgggaattctctctttaagactgtaagt 483
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                                                     Local Similarity
les 70; Conserv
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                                                                Score 40; DB 7; Length 787; Pred. No. 4.7;
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                                             Mismatches
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                                                 53;
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; Sequence 325093, Application US/10027632
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,358
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US-10-027-632-174396
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LENGTH: 787
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Best Local :
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                       CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/218,006
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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; ORGANISM: Human
US-10-027-632-325093
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CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 653

Prior Application removed - See File Wrapper or Software: Patentin Ver. 2.0

SEQ ID NO 632

LENGTH: 6573
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SEQ ID NO 325093
LENGTH: 787
                                                                                                                                                                                                               5.6%;
Best Local Similarity 47.9%;
Matches 115; Conservation
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
4012 gtttttcgatgtgctgctggattcaatttgccagtattttattgaggatttttgcatcaa 4071
                                                                           3952 attgatttgcatatgctgaaccagccttgcattcctagggatgaagccaacttgatcatg 4011
                                                                                                                                                   3892 tctatcgagataatcatgtggtttttgtcattggttctgtttatgtgatggattacgttt 3951
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OR FILING DATE: 2000-04-20
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR FILING DATE: 1999-11-23
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                                                                                               418 attgtcacacagaaaaggaaactgccttgtctccccttccgggaattctctcttttaagact 477
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Local Similarity 55.6%;
                                   FILING DATE:
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                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 8;
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-125-540-561
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                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ05C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
CURRENT FILING DATE: 2002-06-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 384
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 375
LENGTH: 6573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 375, Application US/10158057 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.6%; Score 40; Best Local Similarity 47.9%; Pred. No.
                                                                                            Query Match 5.6%;
Best Local Similarity 47.9%;
Matches 115; Conservative
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT2.14C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/125,540
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                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2622 ATTGATTTGCATATGCTGAACCAGCCTTGCATTCCTAGGGATGAAGCCAACTTGATCATG 2563
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3892 tctatcgagataatcatgtggtttttgtcattggttctgtttatgtgatggattacgttt 3951
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                                                                                                                        Score 40; D. Pred. No. 8;
                                                                                                      Mismatches 125;
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          Sequence 971, Application US/10035832
GENERAL INFORMATION:
APPLICANT: MORTIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
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CURRENT FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR ETILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR ETLING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,576
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                      1960 tgcaacctctgcct 1973
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  2002-07-22
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PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PatentIn version 3.1
SEQ ID NO 971
LENGTH: 30828
27592 tototgtgtagccctggctgacctggcactcactttgt 27629
                                                                       PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (30603)..(30828)
OTHER INFORMATION: "n" at positions 30603 thru 30828 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (22853)..(22872)
OTHER INFORMATION: "n" at positions 22853 thru 22872 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (15334)..(15753)
OTHER INFORMATION: "n" at positions 15334 thru 15753 can be any base
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NAME/KEY: misc_feature
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                       530 ttcttcttttgccctttcttagcttgcactcccatggt 567
                                                                                             470 ttaagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctct 529
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Pred. No. 15;
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Search completed: September 8, 2002, 01:10:14 Job time: 37092 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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             537
298.4
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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376
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AV715411
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AA047220
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             BI838027
BG659530
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1148.320 Million cell updates/sec
                                                               H84298 ys95e09.s1
H86126 ys94g08.s1
AA018441 ze50a08.s1
H86544 yt04f01.s1
R85827 yq22g10.s1
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AA0566275 zf53q03.s
AA011028 ze34d02.s
AA047220 zf49e11.s
AA057418 zf59h03.s
AA020992 ze65f07.s
                                       AL540709 AL540709
AV715411 AV715411
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BI838027 603083875
BG659530 TGESTZYA2
BF569266 602185634
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## ALIGNMENTS

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COMMENT
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BI763679/c
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                                                                                                                                                                                                                                                                                                          source
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: MGC clone distribution information can
Clone distribution: MGC clone distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM11474 row: e column: 17
                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop:
/note-Torgan: pooled colon, kidney, stomach; Vector: /note-Torgan: pooled colon, kidney, stomach; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is
                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:5189752"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                              /clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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REFERENCE
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          AAUJSD53 603 bp mRNA linear EST
Zf55b04.s1 Soares retina N2b4HR Homo sapiens cDNA clone
TMAGE:380815 3', mRNA sequence.
                                                                                                                                                                                                                                        AA058563.1 GI:1551370
EST.
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 74.6%;
Similarity 98.9%;
                                                                                                                                  (bases 1 to 603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 2.6e-89;
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DEFINITION
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JOURNAL
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                                                                                                                          601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
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                                                                                                                                                                                                                                                                  CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTTGGTGG
                                                                                                                                                                                                                                                                                                                                                                      2f3g03.sl Soares retina N2b4HR Homo sapiens cDNA AN056275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.linl.gov) for Insert Length: 921 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation and analysis of 280,000 human expressed sequence tags genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="retina"
/dev_stage="55 year o
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/clone="IMAGE:380815"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.48;
99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 298.4; DB 9; Pred. No. 2.1e-45;
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ACCESSION

AA056275

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241 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCANAGAGACGTG 300

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REFERENCE
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661 gttttgaaaagtccctcgctcagaaatgccagcttgcagatgg¢taatcaaagagacgtg 720
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                                                                                                                                               601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
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EST.
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1. (bases 1 to 577)
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The WashU-Merck EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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//dev_stage="55 year old"
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//lab_host="DH10
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                                                                                        1 GTCNCACAGAAAAAGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTNGT 60
                                                                                                                                                                                                    Local Similarity
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Hillier, L., Clark, N., Dubuque, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Merck EST Project
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
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                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. " 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:1277412"
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/dev_stage="55_year old"
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/clone="IMAGE:360867"
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                                                                                                                                                                                                  39.8%; Score 286.4; DB 9; Length 442; 99.0%; Pred. No. 3.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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of Toronto. Library constructed by Bento
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 agtegetgectgagtggtttcattttgtttttgtttttctgecettetetttttttttg 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAAGATGGCTAATCAAAGAGACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 447)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="55 year old"
//lab_host="DH10B (amplcillin resistant)"
//lab
                                                                                                                                                                 /tissue_type="retina"
/dev_stage="55 year c
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:381269"
                                                                                                                                                                                                                                                                   /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:1289526"
                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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99.3%;
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Pred No. 3.4e-43;
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BASE COUNT
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                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                              TITLE
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467 bp mRNA | linear EST 30-JAN-19-
ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:363877 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, M., M., Mardis, E., Moore, B., Moris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
                                                                                                                                      Genome Res. 6 (9),
97044478
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA020992.1 GI:1484745
                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                           Washington University School of Medicine |
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                   Contact: Wilson RK
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                   (bases 1 to 467)
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                       est@watson.wustl.edu
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1 109 c 107 g 133 t
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 Mismatches

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Pred. No. 5.3e-43;
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                                                                                                  ORGANISM
                                    AUTHORS
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High quality sequence stop: 265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 833 Std Error: 0.00
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 376)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Soares, M., Tan, F., Trevaskis, E., Waterston Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
                                                                                                                                                                                              ys95e09.s1 Soares retina N2b5HR Homo sapiens cDNA clone
                                                                                                                                                                                                                  H84298
                                                                                                                                                 H84298.1 GI:1062969
                                                                                                                                                                                 IMAGE: 222568 3', mRNA sequence.
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111 c 119 g 122 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
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/clone="IMAGE:363877"
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Louis, MO 63108

Hawkins, M., Holman

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Matches 270;
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                                                                                                             691 agcttgcagatggctaatcaaagagacgtg 720
                                                                                                 241 AGCTTGCAGATGGCTAATCAAAGAGACGTG 270
                                                                                                                                               181 CTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCC
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                                        H86126
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 881 Std Error: 0.00
Seq primer: Promega -21m13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                74 a
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                             Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="retina"
/dev_stage="55 year old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares retina N2b5HR"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:222568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:3851329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 270; DB 10; 100.0%; Pred. No. 3.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
626 ggcgcctattattggccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaa 685
                                           506 tyttttgtttttctgcccttctctttcttctttttgccctttctttagcctttgcacttcccatg 565
                                                                                                                                                source
                                                                             61 TGTTTTTTTTTTCTGCCCTTCTCTTTCTTTTTTGCCCTTTCTTAGCTTGCACTCCCATG 120
                                                                                                                                 1 GTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTT 60
                                                                                                                                                                                                            Local
                           270;
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 378.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 398)
Hillier,L., Clark,N., Dubuque,T., Elliston,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE:222494 3', mRNA sequence H86126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H86126.1 GI:1067705
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:3851255"
/db_xref="taxon:9606"
/clone="IMAGE:222494"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="retina"
/dev_stage="55 year c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares retina N2b5HR"
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                                                                                                                                                                                                        36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1800
                                                                                                                                                                                          0,
                                                                                                                                                                                                   Score 259; DB 10; Pred. No. 3.9e-38;
                                                                                                                                                                                        Mismatches
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Length 398; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ATGCCAGCTTGCAGGATGGCTAATCAAAGAG 271
ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 bp mRNA linear EST ze50a08.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362390 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 244.
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314 286 1810
                                                                                                                                            59 a
                                                                                                                                                         Conservative
                                                                                                                                           Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1279093"
                                                                                                                                                                                                                                                                                                                                                        /tissue_type="retina"
/dev_stage="55 year old"
                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:362390"
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                                                                      99.6%;
                                                           0;
                                                        Score 254.4; DB 9; Length 297; Pred. No. 2.9e-37; Indels 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcctgt 662
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 882 Std E
Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 882 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
High quality sequence stops: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 361.
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: PT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primer [5', strand cDNA wa
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/db_xref="GDB:3854355"
/db_xref="taxon:9606"
/clone="IMAGE:223321"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares retina N2b5HR"
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                                                                                                                                                                         Email: est@watson.wustl.edu
Insert Size: 958
High quality sequence stops: 269
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bassa 1 to 419)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                               High quality sequence stop: 269
                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       v922910.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:274746 3', mRNA sequence.
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             /tissue_type="retina"
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                                                 /sex="male"
                                                          /clone_lib="Soares retina N2b4HR'
                                                                                                      /db_xref="GDB:3798432"
                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL540709 LTI_FL002_PL1 Homo sapiens
                                                                                                                                                                                                                                                                   Email: segref@genoscope.cns.fr,
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                                                   /Note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                          /clone_lib="LTI_FL002_PL1"
/lab_host="DH108"
                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                               /clone="CS0DE002YN18"
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99.5%;
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Pred. No. 9.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear EST 16-FEB-2001 s cDNA clone CS0DE002YN18 5 prime
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294 taggamatamgtcmgcaccgmagcagtggttmagccggmaggctcggmagamacggcacct 353
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Chinese National Human Genome Center at Shanghai
S51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801912(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y!, Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Ḥi,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                   Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
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                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="DCBAUC01"
                                                                                                                                                         /note="Vector: pTriplEx2; Site_1: 141 c 156 g 189 t
                                                                                                                                                                                            /dev_stage="mature"
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                                                                                                                                                                                                                              /cell_type="dendritic cells"
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                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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ne DCBAUC01 5', mRNA sequence
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                    359 ttctcqaaaaagttatatgggggctgaatgagcttctggaggcttgtttaccgtttttta 418
                                                                                                               299 aataagtcagcaccgaagcagtggttaagccggagggctcggaagaacggcaccttttct 358
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61 TTCTCGAAAAAGTTATATGGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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BI838027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                   Similarity
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/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pcMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
pcMV-SPORT6; Site_1: Spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5222802"
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BF835617 RC4-HT089
BF994308 CM2-GN016
AZ719811 RPCI-24-1
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Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.Chin;
Tel: 0086-571-86892051
Fax: 0086-571-86961325
                                                                                                              Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

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High-efficiency full-length cDNA cloning. Methods Enzymol. 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="4930501C15"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
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94.78;
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Pred. No. 1.9e+02;
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                                        Zhejiang, P.R.China
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                                                                                                                                                                                                                                                                                                                                              Tel: 212 327 8085
Fax: 212 327 8685
Plate: S10-8 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.

1 (bases 1 to 677)
Altmann,C.R., Bell,E., Sczyrba,A., Pun,J., Bekiranov,S., Gaasterland,T. and BrivanLou,A.H.
Microarray-based analysis of early development in Xenopus Dev. Biol. 236 (1), 64-75 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Molecular Vertebrate Embryology The Rockefeller University
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brivanlou, AH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG410123 677 bp mRNA linear EST ul-AFK-ZUUL S10-8-A10 Stage 10+ Gastrula Library Xenopus laevis cDNA 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21349872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                       1230 York Avenue, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     African clawed frog.
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                                                                                                                 197
         Conservative
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                                                                                                                            translation initiation factor 4AIII. Development 124, 4235-4242."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laevis
                                                                                                                                                    /note-"Vector: pDH105/CS2++; Site_1: Sal I; Site_2: Not I Weinstein.D.C., Honore,E., and Hemmati-Brivanlou,A. (1997) Epidermal induction and inhibition of neural fate by
                                                                                                                                                                                                                                 /clone_lib="Stage 10+ Gastrula Library"
/dev_stage="10 - 10.5"
                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                  /lab_host="DH5alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: psport2"
88 c 109 g 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Oryza sativa mature leaf library induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4530"
/clone="U013C07"
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                       87.0%;
94.7%;
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94.7%;
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                    Score 17.4; DB 10
Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus.
1 (bases 1 to 735)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Normalization and subtraction of rapid discovery of new
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., A. and
N., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muramatsu,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Aizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="al30029G22"
                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                /dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                clone_lib="RIKEN full-length enriched, 16 days neonate"
                                                                                                                                                                   /tissue_type="thymus"
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                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                         This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TICR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG-ND-165J5.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165J5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 вн393256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 796)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus Direct Submission of BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               вн393256.1 GI:17339397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH39325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other_GSSs: AG-ND-165J5 TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence.
                                                                                                                                                                                   Seq primer: M13 For Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
                                                                                                                                                                                                                            partial digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 a
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301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization cap-trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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        /clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: pECBAC1; Site_1: HindIII"
                                                                /clone="AG-ND-165J5"
                                                                               /db_xref="taxon:7165"
                                                                                                                        /organism="Anopheles gambiae"
                                                                                                                                                                 Location/Qualifiers
                                                                                                           /strain="PEST
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94.7%;

 Mismatches

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Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gardner, M. and Loftus, B.J.
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KEYWORDS
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                                                                                                                                                                                                                                                                   59 GATGCCCAAACTGTTTT 75
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Ocal Similarity 94.7%;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Homo sapiens
                                                                                                                                              AL551725 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI062YL18
                                                                                                       AL551725.1 GI:12889952
                                                                                                                                        prime, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Genoscope
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manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: placenta"
/note="Vector: placenta"
/note="Vector: placenta"
/note="Vector: placenta"
/note="Vector: placenta"
/note="vector: placenta"
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
http://fulllength.invitrogen.com"
18 others
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/db_xref="taxon:9606"
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/clone_lib="LTI_NFL006_PL2"
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                                                                                                                                                                                                                                                                                                                                                      85.0%; Score 17; DB 9; 100.0%; Pred. No. 3.7e+(
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
          Class: plasmid ends
High quality sequence stop: 200.
                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0564 row: H column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                   Contact: Robert B.
                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                            plasmid inserts
                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1M0564H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564H07 F, DNA sequence.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                                                                                                                        USA
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261 c 212 g 235 t 4 others
                                                                                                                                                                                          ... Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI062YL18"
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                                                                                                  Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae; Mus.
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   את אייטיטט 291 bp mRNA | linear E
zu64a03.rl Soares_testis_NHT Homo sapiens cDNA clone
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA400303.1 GI:2054192
                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 205.
                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine |
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwn42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                            est@watson.wustl.edu
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564H07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
/organism="Homo sapiens"
/db_xref="GDB:5929684"
/db_xref="taxon:9606"
                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%;
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Pred. No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RC4-HT0890-151100-017-ell HT0890 Homo sapiens cDNA, mRNA sequence.
BF835617
                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-HT0890-
151100-017-ell&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson, A.J.
                                                                                                                                                                                            High quality sequence start: 17
High quality sequence stop: 302.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pouble-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "a 62 c 46 g 103 t
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                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="0rgan: head_neck; Vector: puc18; Site_1: SmaI; /note="0rgan: head_neck; Vector: puc18; Site_1: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application
                                                                        /dev_stage="Adult"
                                                                                                 /clone_lib="HT0890"
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=CM2&t2=CM2-GN0165-
021100-487-a03&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., 2ago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
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1 (bases 1 to 314)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence start: 8 quality sequence stop: 143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                 /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI  
    Site_2: SmaI; A mini-library was made by cloning  
    products derived from ORESTES PCR (U.S. Letters Patent  
    application No. 196,716 - Ludwig Institute for Cancer  
    Research) profiles into the puc 18 vector. Reverse  
    transcription of tissue mRNA and cDNA amplification were  
    performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0165"
                                                                                                                                                                                                                                                                                                      /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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54 c 65 g 107 t
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90.0%;
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                        Score 16.8;
Pred. No.
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Pred. No. 4e
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  4e+02;
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                     DB 10;
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                                                                                                                                                   AGAAATGCCCAAAGTGTTTT 110
BB508020
BB508020 RIKEN full-length enriched, 10 days lactation, adul female mammary gland Mus musculus cDNA clone D730015N05, mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 161 row: H column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theo,S., Nierman,W., Malek,J., Shatsman,S., AN Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="RPCI-24-161H14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2)/ 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) | Carninci,P. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High-efficiency full-length cDNA cloning.
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was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." s 53 c 68 g 113 t
                                                                                          Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="mammary gland"
/dev_stage="10 days lactation, adult"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="D730015N05"
/clone_lib="RIKEN full-length enriched, 10 days lactation,
                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adult female mammary gland"
/sex="female"
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                              RESULT 15
AW879474/c
LOCUS
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                                                                                                                  221 AGAGATGCCTAAAATGTTTT 202
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HUM099E06A Clontech human fetal brain polyA+ mRNA (#6535) Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens cDNA clone GEN-099E06 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           Otsuka Pharmaceutical Co., Itd
463-10 kagasuno Kawauchi-cho,
Tel: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaic,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
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Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 365)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AWO/94/4
PMO-OT0019-180400-003-f04 OT0019 Homo sapiens cDNA,
AW879474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Otsuka GEN Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tsutomu Fujiwara
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                  /clone="GEN-099E06"
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Pred. No. 4e+02;
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                                          EST 23-MAY-2000
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Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 377)

Homo sapiens

EST

AW879474.1 GI:8041484

mRNA sequence.

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Search completed: September 7, 2002, 14:51:20 Job time: 16179 sec
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                                                                                                               341 AGAGACGCCCAAACTGGTTT 322
                                                                                                                                                                                                                 Local Similarity hes 18; Conserv
                                                                                                                                       1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=PM0-OT0019-180
400-003-f046t3=2000-04-186t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 377.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                         94 a
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                   /note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                84.0%; Score 16.8; DB 9; Length 377; 90.0%; Pred. No. 4.2e+02; tive 0; Mismatches 2; Indels (
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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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 score greater than or equal to the score of the result well and is derived by analysis of the total score distribution.
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score greater than or equal to the score of the result being printed,
Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

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5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
                                                                                                                                                                                                                                                                                                       Query
Match Length DB
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Gapop 10.0 , Gapext 1.0
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  2036664 segs, 1522705736 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
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34547
                                                 US-10-035-832-1262
US-09-975-254-17065
US-09-975-254-27065
US-09-975-254-2768-2716
US-09-9785-2768-2716
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US-09-985-2768-4980
US-09-918-995-1368-4980
US-09-986-492-185589
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                        Sequence 7482, Ap
Sequence 7482, Ap
Sequence 17065, Ap
Sequence 205156,
Sequence 20716, Ap
Sequence 2716, Ap
Sequence 21743, A
Sequence 21743, A
Sequence 27588, A
Sequence 28808, A
Sequence 28808, A
Sequence 41983, A
Sequence 43780, A
Sequence 43780, A
Sequence 43780, A
Sequence 1867, Ap
Sequence 1867, Ap
Sequence 5950, A
Sequence 6997, Ap
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                Sequence
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RESULT 2 US-10-105-299-7482/c

Sequence 7482, Application US/10105299 GENERAL INFORMATION: APPLICANT: Rosen, et. al

TILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
NUMBER OF SEQ ID NOS: 15197
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7482
LENGTH: 34547

ORGANISM: Homo sapiens

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1 agagatgcccaaactgtttt 20 ||||||||||||||||||||||| 8037 agagatgcccaaactgtttt 8056

Query M Best Lo Matches	RESULT 1 US-10-035-832 Sequence 12 Sequence 12 GEMERAL INF APPLICANT: APPLICANT: FILE REFER CURRENT FI FRIOR FILE PRIOR APPL PRIOR FILI PRIOR APPL PRIOR FILI PRIOR F		C C C C C C C C C C C C C C C C C C C
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₽.	1 1832-1262 Application INFORMATION: ANT: MOSTIS, DAVID ANT: ENGELHARD, ET OF INVENTION: NOVEL EFFERENCE: A-71249/R T APPLICATION NUMBER: T APPLICATION NUMBER: T FILING DATE: 2000 APPLICATION NUMBER: FILING DATE: 2001-0 FILING DATE: 2001-0 FOLICATION NUMBER: FILING DATE: 2001-0 FOLICATION NUMBER: FILING DATE: 2001-0 OF SEQ ID NOS: 161 RE: PATENTIN VETSIO NO 1262 H: 45121 DNA UISM: Homo sapiens -832-1262		79.0 79.0 79.0 79.0 79.0 79.0 79.0 79.0
100 larity 100 Conservative	1-832-1262 ce 1262, Application US/100 ce 1262, Application US/100 L INFORMATION: L INFORMATION: David CANT: MOTIS, David CANT: Engelhard, Eric OF INVENTION: NOVEL COMPOS REFERENCE: A-71249/RMS/DCF INT APPLICATION NUMBER: US 09/ FILING DATE: 2002-07-22 APPLICATION NUMBER: US 09/ FILING DATE: 2001-012-22 R APPLICATION NUMBER: US 09/ FILING DATE: 2001-03-02 R OF SEQ ID NOS: 1613 R OF SEQ ID NOS: 1613 ARE: Patentin version 3.1 DNA ANISM: Homo sapiens 35-832-1262		1157 1157 1157 1157 1195 1195 1195 1195
.09	US/1 tc COMP 4S/DC 4S/DC 8: US 2-07- 2-07- 0''' 0'''' 0'''' 0''''' 0''''''''''		55566778557777
Score 20; DB 6; Le ; Pred. No. 1.9; 0; Mismatches 0;	2-1262 2-1262 262, Application US/10035832 FORMATION:  ** MOTT'S, David  **: Engelhard, Eric INVENTION: NOVEL COMPOSITIONS AND METHODS FOR PLICATION NUMBER: US/10/035,832 **TLING DATE: 2002-07-22 **TLING DATE: 2002-07-23 **ILICATION NUMBER: US 09/747,377 **LICATION NUMBER: US 09/747,377 **LICATION NUMBER: US 09/747,377 **LICATION NUMBER: US 09/798,586 **ING DATE: 2000-03-02 **SEQ ID NOS: 1613 **ING DATE: 2001-03-02 **SEQ ID NOS: 1613 **IPA TABLE TO THE TAB	ALIGNMENTS	PCT-US02-09257-91 PCT-US02-09370-140 PCT-US02-09370-140 PCT-US02-0992-85 US-10-105-299-180 US-09-919-002-1295 PCT-US02-23913-396 US-10-102-8233-396 US-10-114-678A-878 US-10-011-095-1 US-10-179-131-3023 US-09-620-325-172 US-60-360-039-45839 US-10-011-667A-6 US-10-010-667A-6 US-10-013-832-1214 US-10-015-832-1214 US-10-015-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-10-05-832-1214 US-09-396-196G-54633 US-09-396-196G-54633 US-09-396-196G-54634 US-09-396-196G-54634
Length 45121; Indels 0; Gaps	R CANCER		Sequence 91, Appl Sequence 140, App Sequence 185, Appl Sequence 195, App Sequence 396, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 172, App Sequence 45839, A Sequence 1214, App Sequence 1214, App Sequence 1214, App Sequence 1214, App Sequence 202, App Sequence 54633, A Sequence 54634, A Sequence 54634, A Sequence 54634, A Sequence 1291, App Sequence 12

US-10-105-299-7482

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: LENGTH: 253
: TYPE: DNA
: ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: 700733864H1
US-09-975-254-2234
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US-09-975-254-2234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; Glycine max; ORGANISM: Glycine max; OTHER INFORMATION: Clone ID: 700953921H1 US-09-975-254-17065
                                                                                                                                                                                       APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)8
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION NUMBER: US/09/263,191
NUMBER: OF SEQ ID NOS: 31255
SEQ ID NO 2234
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SEQ ID NO 17065
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
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APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(1539)B
FILE REFERENCE: 38-21(1539)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 251
1 agagatgcccaaactgtttt 20
                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 agagattcccaaacttttt 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                        2234, Application US/09975254
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                                                 Conservative
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                                                             84.0%;
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100.0%; Pred. No.
tive 0; Mismatc
                                                           Score 16.8;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8;
Pred. No. 4
                                            Mismatches
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                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 34547; 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                            2;
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                                                                       Length 253;
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                                       Gaps
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APPLICANT: Stuve, APPLICANT: Mullaby, Sara J.
APPLICANT: Mullaby, Sara J.
APPLICANT: Mullaby, Sara J.
APPLICANT: Mughton, Rebecca E.
TITLE OF INVENTION: FOLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: NOVEMBER 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR APPLICATION NUMBER: 08/395,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITTLE OF INVENTION: Polymorphisms in the Human Genome
CURRENT EFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR RILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20774, Application US/09540210B GENERAL INFORMATION:
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                                                                                                         PRIOR FILING DATE: September 27, 1991
PRIOR APPLICATION NUMBER: 60,0005,526
PRIOR FILING DATE: September 29, 1992
PRIOR APPLICATION NUMBER: 08,824,029
PRIOR FILING DATE: MARCH 25, 1997
PRIOR APPLICATION NUMBER: 05, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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SEQ ID NO 205156
                                                                                                                                                                                                           PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 agaaatgtccaaactgtttt 89
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     APPLICATION NUMBER: 60/014,010 FILING DATE: March 25, 1996 APPLICATION NUMBER: 08/826,847 FILING DATE: APRIL 10, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for Windows Version 4.0
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: 08/826,847
10, 1997
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Pred. No. 4
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PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR FILING DATE: June 24, 1997
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR PELICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR FILING DATE: June 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/052,751
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IOR FILING DATE: June 25, 1996
IOR APPLICATION NUMBER: 60/03, 802
IOR FILING DATE: July 31, 1997
IOR FILING DATE: July 31, 1996
IOR FILING DATE: July 31, 1997
IOR FILING DATE
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IOR APPLICATION NUMBER: 08/905,881
IOR APPLICATION NUMBER: 08/905,881
IOR APPLICATION NUMBER: 60/025,204
IOR FILING DATE: August 1, 1997
IOR APPLICATION NUMBER: 60/025,204
IOR FILING DATE: August 1, 1996
IOR APPLICATION NUMBER: 08/903,471
IOR FILING DATE: July 30, 1997
IOR APPLICATION NUMBER: 60/025,478
IOR APPLICATION NUMBER: 60/025,478
IOR APPLICATION NUMBER: 08/903,556
IOR FILING DATE: July 31, 1996
IOR FILING DATE: July 31, 1997
IOR APPLICATION NUMBER: 60/025,217
IOR FILING DATE: August 22, 1996
IOR APPLICATION NUMBER: 08/937,142
IOR APPLICATION NUMBER: 08/937,143
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OR FILING DATE: October 30, 1996
OR APPLICATION NUMBER: 08/826,847
OR FILING DATE: April 10, 1997
OR APPLICATION NUMBER: 60/015,533
OR FILING DATE: April 10, 1996
OR APPLICATION NUMBER: 08/755,524
OR APPLICATION NUMBER: 08/755,524
OR FILING DATE: NOVEMBER 22, 1996
OR FILING DATE: NOVEMBER 22, 1996
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APPLICATION NUMBER: 60/039,325
FILING DATE: February 13, 1997
APPLICATION NUMBER: 09/035,172
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FILING DATE: November 22, 1995
APPLICATION NUMBER: 09/21,031
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APPLICATION NUMBER: 08/960,746
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FILING DATE: July 1, 1997
APPLICATION NUMBER: 09/094,079
FILING DATE: June 9, 1998
APPLICATION NUMBER: 60/049,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/040,199
FILING DATE: March 14, 1997
APPLICATION NUMBER: 09/050,817
FILING DATE: March 30, 1998
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July 31, 195,
TMRER: 60/023,308
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: LOCATION: 31, 71, 74,
: OTHER INFORMATION: a,
US-09-540-210B-20774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-785-276A-2716
                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: 158, 166, 285
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-2716
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
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NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 20774
LENGTH: 289
    B
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                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MONABAN, JOHN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LOENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                 Matches
                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Inc
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                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPOLATION | 101 GAGATGCCCACACTGTTGT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.0%;
Local Similarity 89.5%;
nes 17; Conservation
172 gagaagcccaaactgcttt 190
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                       2 gagatgcccaaactgtttt 20
                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                         364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                       79.0%;
89.5%;
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Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                    Score 15.8; DB 5;
Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
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                                                                                                                                Length 364;
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RESULT

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CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11885
LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-785-276A-21743/c
; Sequence 21743, Application US/09785276A
                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/2189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
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                                                                               NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21743
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: 00/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/255,281 PRIOR FILING DATE: 2000-12-13
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schlegel. Robert
APPLICANT: Bindege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: MORANA, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007B
                                                        ENGTH: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 gagaagcccaaactgcttt 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
mes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 gagatgcccaaactgtttt 20
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                                                                                                                                                         2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%; Score 15.8; DB 5; 89.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Sequence 27588, Application US/09785276A

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
ITITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
ITITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: 50/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
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; ORGANISM: Homo sapiens
US-09-785-276A-22947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183/319
PRIOR APPLICATION NUMBER: 60/189/862
PRIOR APPLICATION NUMBER: 60/207/454
PRIOR APPLICATION NUMBER: 60/207/454
PRIOR APPLICATION NUMBER: 60/207/454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211/314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219/007
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
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PRIOR APPLICATION NUMBER: 60/207,454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/785,276A CURRENT FILING DATE: 2001-02-16
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nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 gagatgcccaaactgtttt 20
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89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 5; Length 440;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; DB 5;
1.6e+02;
ches 2;
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; TYPE: DNA ; ORGANISM: Homo sapiens US-09-785-276A-27588
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PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-12-13

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232
                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Homo sapiens US-09-785-276A-28808
US-09-785-276A-33057

Sequence 33057, Application US/09785276A

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 27588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MONAĥAN, JOHN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRÉVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
EILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-0-17
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlegel.
APPLICANT: Endege, I
APPLICANT: Monahan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/189,862
PRIOR ETLING DATE: 2000-03-16
PRIOR PPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
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308 GAGAAGCCCCAAACTGCTTT 290
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                                                                                                                                                                                                                                                                       Local Similarity
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89.5%; Pred. No. 1.6e+02;
vative 0; Mismatches 2;
                                                                                                                                                                                                                                                                          79.0%;
                                                                                                                                                                                                                                                                       Score 15.8;
Pred. No. 1.
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                            8; DB 5;
1.6e+02;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-785-276A-33057
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-785-276A-41983
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41983, Application US/09785276A
                                                                                                 NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41983
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
FILE REFERENCE: MRI-007B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
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PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
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APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LOENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR ADDITORMICS
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/785,276A CURRENT FILING DATE: 2001-02-16
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                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/255,281 PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/219,007
                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-07-18
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                                                                                LENGTH: 451
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Local Similarity 89.5%;
hes 17; Conservative
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US-09-785-276A-43780

US-09-785-276A-43780

Sequence 43780, Application US/09785276A

Sequence 43780, Application US/09785276A

APPLICANT: Schlegel. Robert

APPLICANT: Schlegel. Robert

APPLICANT: Monahan, John

ITILE OF INVENTION: HUMAN PROSITIONS, KITS, AND METHODS FOR

ITILE OF INVENTION: HUMAN PROSITIONS, KITS, AND THERAPY OF

FILE REFERENCE: MRI-0079

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US/09/785,276A

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/283,319

PRIOR APPLICATION NUMBER: 60/283,319

PRIOR APPLICATION NUMBER: 60/21,314

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR APPLICATION NUMBER: 60/255,281

PRIOR APPLICATION NUMBER: 60/251,314

PRIOR APPLICATION NUMBER: 60/251,314
Search completed: September 8, 2002, 01:09:18 Job time: 37036 sec
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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174 gagaagcccaaactgcttt 192
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels (
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pending_Patents_NA_Main:*
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/ Cgn2_6/ptodata/2/pna/US000C_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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16.8 16.8 16.8 16.8 16.8			Score
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Sequence 17065, A Sequence 108604, Sequence 108604, Sequence 2234, Ap Sequence 6446, Ap Sequence 458, App Sequence 458, App	5377 5377 3905, 3905 3905 6288	sequence 12, Appli sequence 26, Appl sequence 26, Appli sequence 1, Appli sequence 1, Appli sequence 10, Appli sequence 719, App sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 50130, A sequence 2703, Ap sequence 82703, Ap sequence 82703, Ap sequence 5331, Ap sequence 158, App sequence 158, App sequence 158, App	3   5

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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 1909-10-18
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
                                                                                                                                                                                                                                             US-09-834-291-18
                                   NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-834-291-12
                                                                                                                                                                                                                 Sequence 18, Application US/09834291 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 20
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
-09-834-291-12
                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE9/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
RUMBER OF SEQ ID NOS: 32
                              LENGTH: 40
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17 US-09-342-216-31
17 US-09-342-216A-31
17 US-09-908-601-31
34 US-09-912-292-1183
15 US-09-912-292-1183
15 US-09-974-300-1452
17 US-09-304-517A-249988
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6 US-09-283-466-6496
11 US-60-125-8118-6768
PCT-US02-03987-6707
11 US-09-815-242-6707
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 40
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-26
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4
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GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/0343
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-0-16
PRIOR FILING DATE: 1998-0-16
PRIOR FILING DATE: 1998-0-16
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Query Match 100.0%; Score 20; DB 32; Length 2827; Best Local Similarity 100.0%; Pred. No. 18; Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 4
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PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
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CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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Best Local Similarity
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US-09-834-291-1
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US-09-834-291-1
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                                                                                                                                                                                                                                                                 LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-722-10
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                  US-09-910-943-719/c
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PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
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CURRENT FILING DATE: 2001-08-21
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APPLICANT: MOITIS, David
APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
APPLICANT: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILLE REFERENCE: A-71171/RWS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEC ID NOS: 301
NUMBER OF SEC ID NOS: 301
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Sequence 719, Application US/09910943
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                                                                                           8037 agagatgcccaaactgtttt 8056
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Length 3212;

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; LOCATION: (1)..(732) ; OTHER INFORMATION: n may be a or g or c or t/u US-09-910-943-719
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APPLICANT: Altman, Curtis
APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/IG148US1
FULE REPERENCE: 7529/IG148US1
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
SEQ ID NO 719
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                                                                               Sequence 1, Application US/09438185
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Davis, Ronald
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
FITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FITLE REFERENCE: 018941-000411US
                                                                                                                                                                                                                                                                                                                                                                   Db 23498 AGAGATGCCCAAACTGATT 23480
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
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Best Local Similarity
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TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
TITLE OF INVENTION: Sequences and Uses Thereof
FILE REFERENCE: CL000284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
CURRENT APPLICATION NUMBER: US/99/438,185
CURRENT FILING DATE: 1999-11-11
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
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TYPE: DNA
ORGANISM: Drosophila
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1999-04-08

US 60/128,606

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APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Chlamydia pneumoniae Genome Sequence
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR APPLICATION NUMBER: US 60/128,606
NUMBER OF SEQ ID NOS: 1074
SOFTMARE: FastSEQ for Windows Version 3.0
LENGTH: 1930730
                                                                                                                                                                                                                                                                   US-09-815-264-56014/c
; Sequence 56014, Application US/09815264
; GENERAL INFORMATION:
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; ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1
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APPLICANT: WCININCH, James
APPLICANT: WL, Wei
TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
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APPLICANT:
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/ ORGANISM: Chlamydia pneumoniae
US-09-438-185-1
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                                                                                                                                                                                                                             APPLICANT: Boukharov, Andrey A. APPLICANT: Cao, Yongwei
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PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 107
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Dotson, Stanton B.
Koshi, Jeffrey M.
Kovalic, David K.
                                                                                                                                                      Liu, Jingdong
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94.7%;
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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-2703
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; LENGTH: 7865
; TYPE: DNA
; ORGANISM: OTYZA SATIVA
US-09-620-392-50130
Ouery Match 85.0%; Score 17; DB 28; Length 7865; Best Local Similarity 100.0%; Pred. No. 8e+02; Matches 17; Conservative 0; Mismatches 0; Indels
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SEQ ID NO 2703
LENGTH: 7865
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US-09-815-264-56014
                                                                                                                                                                                   FILE REFERENCE: 38-21(51237)F
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT FILING DATE: 2000-10-31
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TITLE OF INVENTION: P
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 56014
LENGTH: 1501
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Best Local (
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les 17; Conserv
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Kovalic, David K.
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; ORGANISM: Oryza sativa
US-09-815-264-82703
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SEQ ID NO 82703
LENGTH: 7865
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FILE REFERENCE: 38-21(51237)G
FURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-04-12 PRIOR APPLICATION NUMBER: PCT. PRIOR FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/833,245
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                                                                       PRIOR APPLICATION NUMBER: PCT/US00/06059
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06042
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              FILING DATE: 2000-03-09
APPLICATION NUMBER: PCT/US00/06014
FILING DATE: 2000-03-09
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APPLICATION NUMBER: PCT/US00/06013
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Kovalic, David K.
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FILING DATE: 2000-03-16
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APPLICATION NUMBER: PCT/US00/06057
FILING DATE: 2000-03-09
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APPLICATION NUMBER: PCT
FILING DATE: 2000-03-16
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APPLICATION NUMBER: PCT/US00/06828
FILING DATE: 2000-03-16
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FILING DATE: 2000-03-22
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          APPLICATION NUMBER: PCT/US00/09067 FILING DATE: 2000-04-06
                                                APPLICATION NUMBER: PCT/US00/08983 FILING DATE: 2000-04-06
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APPLICATION NUMBER: PCT
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FILING DATE: 1999-06-11
APPLICATION NUMBER: US 60/168,665
                                                                     APPLICATION NUMBER: US 60/124,095 FILING DATE: 1999-03-12
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                                               APPLICATION NUMBER: US 60/138,598
                                                                                                                     FILING DATE: 1999-12-03
                                                                                                                                   APPLICATION NUMBER: US 60/168,663
                                                                                                                                                                  FILING DATE: 1999-03-12
                                                                                                                                                                                APPLICATION NUMBER: US 60/124,143
                                                                                                                                                                                                        APPLICATION NUMBER: US 60/168,622 FILING DATE: 1999-12-03
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FILING DATE: 1999-03-12
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FILING DATE: 2000-09-26
APPLICATION NUMBER: PCT/US00/26337
FILING DATE: 2000-09-26
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FILING DATE: 2001-04-27
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FILING DATE: 2000-09-26
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FILING DATE: 2000-06-01
APPLICATION NUMBER: PCT/US00/14973
FILING DATE: 2000-06-01
APPLICATION NUMBER: PCT/US00/14964
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FILING DATE: 2000-06-01
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FILING DATE: 2000-06-01
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FILING DATE: 2000-06-01
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APPLICATION NUMBER: PCT/US00/08980
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FILING DATE: 2000-04-06
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                                                                                         Matches
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Best Local
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PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US 60/168,664
PRIOR FILING DATE: 1999-12-03
30417 AGATGCCCAAACTGTTT 30401
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PRIOR FILING DATE: 1999-03-23
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FILING DATE: 1999-66-11
APPLICATION NUMBER: US 60/168,667
FILING DATE: 1999-12-03
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/138,597 FILING DATE: 1999-06-11
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FILING DATE: 1999-06-11
APPLICATION NUMBER: US 60/168,662
FILING DATE: 1999-12-03
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APPLICATION NUMBER: US 60/125,360
FILING DATE: 1999-03-19
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17; Conserv
                                                                              85.0%; Silarity 100.0%; Silarity 00.0%; Silarity 00.0%; Silarity 0;
                                                                              Score 17; DB 35;
; Pred. No. 1.1e+03;
0; Mismatches 0;
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Search completed: September 7, 2002, 22:31:31 Job time: 43785 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-09-323-873A-1
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US-09-323-873A-1
US-09-323-873A-1
US-09-323-873A-1
US-09-320-61B-15
US-08-460-934-5
US-08-782-118-8
US-08-782-118-8
US-08-782-118-8
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US-09-109-204-2
US-09-109-204-2
US-09-109-204-1
US-09-109-204-5
US-08-473-496-1
US-08-473-496-1
 PCT-US94-05388-3

PCT-US95-09121-1

PCT-US96-07496-3

US-09-217-609A-4

US-08-873-235B-4

US-08-981-690-1

US-09-217-609A-21

US-08-873-235B-21

US-08-466-033-182
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(without alignments)
23.140 Million cell updates/sec
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Sequence 6, Appli
Sequence 7, Appli
Sequence 13, Appl
Sequence 15, Appl
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Sequence 19, Appl
Sequence 5, Appli
Sequence 28, Appl
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Sequence 14, Appl		sequence to, Appr	ر ا د	27,	Sequence 3, Appl1	Sequence 20, APPI	ا ر ا 0	5	Sequence 6, Appli	actacarca rost	10.	Sequence 2, Appli	Sequence 10, April	n .	Sequence 64, Appl	Sequence II, APPI	111	156.	Sequence 182, App	-		Sequence 182, App	Sequence 182, App	

ALIGNMENTS

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; Sequence 3, Application US/08578634C ; patent No. 6025163
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                                                                                                                                                            TELEFAX: (650)493-5550
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPUTER: DOS PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
TITLE OF INVENTION: VIRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 841
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 661 base pairs
                                    FEATURE:
                                                  MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                         TOPOLOGY:
                                                                                                                                                                                                                   TELEPHONE:
NAME/KEY: CDS
LOCATION: 1 .. 660
                                                                                     STRANDEDNESS: double
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                                                                                                                                                                                                 (650)493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                   (650) 493-4935
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RESULT 3
                                     Db 22516 AGAGATTGCCAAACTGTTTT 22535
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                                                                                                      Matches
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                                                                                                                                                                                                                                       TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
NAME: CARRELY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                 1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reeve, Mary Pat TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                 Local Similarity
                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-07A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lexington
STATE: Macon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         567 AGAGTTGCCCAAAGTGTTTT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 agagatgcccaaactgtttt 20
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                                                                                                 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two Militia Drive
                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hawkins, Trevor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reijo, Renee
Saxena, Richa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                        single
                                                                                                              84.0%;
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90.0%; Pred. No. 4.7;
                                                                                              0; Mismatches
                                                                                                              Score 16.8;
Pred. No. 1
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                                                                                                           10;
                                                                                                                      DB 3; Length 43795;
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APPLICANT: ATTHUR B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: Steve Chappell Mitchell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO

FILE REFERENCE: 129.16USU2

CURRENT APPLICATION NUMBER: US/09/323,873A

CURRENT FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Daniel E. Afar

APPLICANT: Rene S. Hubert

APPLICANT: Kahan Leong

APPLICANT: Kahan Leong

APPLICANT: Kathur B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: Douglas C. Saffran

APPLICANT: Steve Chappell Mitchell

TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO

CURRENT APPLICATION NUMBER: US/09/323,873A

CURRENT APPLICATION NUMBER: 60/097,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

COMMEND OF SEG ID NOS: 32
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                                                 Matches
                                                                Query Match
Best Local S
                                                                                                                                                                                                                              SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-323-873A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09323873A Patent No. 6329503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-323-873A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                          ENGTH: 3627
2 gagatgcccaaactgtttt 20
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                                                 11 Similarity
17; Conserv
                                          Conservative
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                                                         79.0%;
89.5%;
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                                  0; Mismatches
                                                         Score 15.8;
Pred. No. 22;
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Pred. No. 18;
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                                                                          DB 4;
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                                    2
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                                                                        Length 3627;
                                    Indels
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                                Gaps
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596 GAGAAGCCCAAACTGCTTT 578

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RESULT 5
US-07-903-047-7/c
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                                                                                                                                                                                                                                                                                        RESULT 6
US-09-111-752-13/c
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                                                                                                                                                                                                                                            Sequence 13, Application US/09111752 Patent No. 6074859
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kajiyama, Naoki
APPLICANT: Nakano, Eiichi
TITLE OF INVENTION: Thermostable Luciferase Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: DNA, And Process For The Preparation Of Thermostable
TITLE OF INVENTION: Luciferase Of Firefly
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA to mRNA
                                                                                                APPLICANT: HIROKAWA, KOZO
APPLICANT: KAJIYAMA, NAOKI
APPLICANT: MURAKAMI, SELJI
TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND
TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                         369 AGAGATGCCTAAACTGT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                             1 agagatgcccaaactgt 17
|||||||||||
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1644 base pairs
NUCLEIC ACID
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7005-048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1644;
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ORGANISM: Luciola lateralis US-09-111-752-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-380-061B-15/c
Sequence 15, Application US/09380061B
Patent No. 6265177
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 08-JUL-CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: VA
                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATION SYSTEM: PC-DOS/MS-DOS

COPTWARE: Patentin Release #1.0, Version #1.25 (EPO)

COURRENT APPLICATION NUMBER: US/09/380,061B

APPLICATION NUMBER: US/09/380,061B

PILING DATE: 25-Aug-1999

CLASSIFICATION: CUNKNOWN>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 AGAGATGCCTAAACTGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SQUIRRELL, DAVID JAMES
WHITE, PETER JOHN
LOWE, CHRISTOPHER ROBIN
LOWE, CHRISTOPHER ROBIN
MURRAY, JAMES AUGUSTUS HENRY
TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22202
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                                                                                                                                                                                                                                                                                                                                                 CITY: ARLINGTON STATE: VIRGINIA
                   APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-ARR-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1644;
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NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER:

124-725

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US-08-460-934-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
             ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,6
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KIKUCHI, MAMORU

APPLICANT: KOYAMA, YASUJI

TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
TITLE OF INVENTION: ANALYSIS METHOD

NUMBER OF SEQUENCES: 14

CORRESSED CORNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                               FILING DATE:
 REFERENCE/DOCKET NUMBER:
                                                                     FILING DATE:
                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                              369 AGAGATGCCTAAACTGT 353
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 agagatgcccaaactgt 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                           22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1644 base pairs
                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUKUDA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATSUMI, HIROKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                UMBER: JP 98857/1995
24-APR-1995
                                                                                                             14-MAR-1995
                                                                                                                                                                                                                         05-JUN-1995
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                                                                                                                       JP 54625/1995
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94.1%;
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               24,618
7126-001-0
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Pred. No. 31;
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US-08-782-118-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08782118 Patent No. 5843746
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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   FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
APPLICATION NUMBER: JP 98857/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: KOYAMA, Y
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                           ZIP: 22202
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                   APPLICATION NUMBER: US 08 FILING DATE: 05-JUN-1995 APPLICATION NUMBER: JP 19 FILING DATE: 27-JUL-1994
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                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 13-JA
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1.1704
OTHER INFORMATION: /note= "Nucleotide sequence of the
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombin
OTHER INFORMATION: plasmid pHLf203 DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                              ARLINGTON
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FUKUDA, SATOSHI
KIKUCHI, MAMORU
KOYAMA, YASUJI
                                                                                                                                                                                                                                                                                                                                                                              USA
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24-APR-1995
                                                                                                                                                                                                                13-JAN-1997
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94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOTINYLATED FIREFLY LUCIFERASE, A GENE FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANALYSIS METHOD
                                                                                                                                                          US 08/460,934
                                                                                                                        JP 193798/1994
                                                                                                                                                                                                                            US/08/782,118
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Pred. No. 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1704;
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US-08-782-118-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIR
TITLE OF INVENTION: FOR BIOTINYLATE
TITLE OF INVENTION: PROCESS FOR PROI
TITLE OF INVENTION: ANALYSIS METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                  FILING UP.... 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
APPLICATION NUMBER: 27-JUL-1994
                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 AGAGATGCCTAAACTGT 413
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double
FILING DATE: 14-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                       FILING DATE: 05-JUN-1995
                                                                                                                                                             APPLICATION NUMBER: US/08/460,934
                      APPLICATION NUMBER: JP 5 FILING DATE: 14-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
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1..1704
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                                                                                                                                                                                                                                                                                                          USA
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Nucleotide sequence of the
biotinylated firefly luciferase gene contained in recombinant
plasmid pHLf203 DNA" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOTINYLATED FIREFLY LUCIFERASE, A GENE
FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
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                                         JP 54625/1995

 Mismatches

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Pred. No. 31;
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; NAME/KEY:
; LOCATION:
US-08-460-934-8
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US-08-782-118-8/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: TATSUM
APPLICANT: FUKUDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-413-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/460,934
APPLICATION NUMBER: US 08/460,934
APPLICATION NUMBER: US 08/460,934
APPLICATION NUMBER: US 08/460,934
APPLICATION NUMBER: US 08/460,934
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 AGAGATGCCTAAACTGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 71:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: OBLON, NORMAN F. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 1..1908 OTHER INFORMATION: /not OTHER INFORMATION: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 77.0%;
Local Similarity 94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 agagatgcccaaactgt 17
                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
FILING DATE: 05-JUN FILING DATE: UP 19 APPLICATION NUMBER: JP 19 APPLICATION NAME: 27-JUL-1994
                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                       FILING DATE:
                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUKUDA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIKUCHI, MAMORU
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                                                                                                                                                                                                                Floppy disk
                                                                                                         13-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "The nucleotide sequence of
the biotinylated firefly luciferas
recombinant plasmid pHLf248 DNA"
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                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                               US/08/782,118
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PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

14-MAR-1995

JP 54625/1995

JP 98857/1995

PRIOR APPLICATION DATA:

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US-08-578-634C-2/c
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GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserv
                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 26-JAN-19
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
TITLE OF INVENTION: VIRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                             MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
                APPLICATION NUMBER:
                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 90
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 71
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                                                                                                                                                                                                         10036
                                                                                                                                                                                                                                                               1155 Avenue of The Americas
                                                                                                                                                                                                                     USA
                                                                                                        Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                26-JAN-1996
                                                                           US/08/578,634C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "The nucleotide sequence of
the biotinylated firefly luciferase gene contained in
recombinant plasmid pHLf248 DNA"
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RESULT 13
US-09-109-204-20/c
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             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20
Patent No.
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                                                   NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
TELEFAX: (650)493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                               TELEX:
                                          TELEFAX: 650-855-0572
                                                                                                                                             FILING DATE
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                              OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                            STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       567 AGAGCTACCCAAAGTGTTTT 548
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                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 17; Conserv
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TYPE: nucleic acid
STRANDEDNESS: double
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NO. 6060250
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                                                                                                                                                                                                                                                                                                                             USA
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Hillman, Jennifer L.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                        Patterson, Change
Patterson, Change
VENTION: HUMAN TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley, Neil C.
Patterson, Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorgone,
                                                                                                                                                                                                                                                                  IBM Compatible
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                                                                                                                                                                                                                                                                                    Diskette
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                                                                                                                                                                                                           US/09/109,204
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A
                                                                               PF-0546 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 668;
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LENGTH:

495 base pairs

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US-09-109-204-19
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                                          US-09-109-204-19
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Patent No. buck-
Tal, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
Query Match
                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: TESTNOTO4
CLONE: 301251T6
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 AGATGGCCAAACTGTATT 328
                                                                  LIBRARY: N/A
                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 agatgcccaaactgtttt 20
                                                                                                                                                                                                                                        NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                 TOPOLOGY:
                                                                                                             STRANDEDNESS:
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                                                         SAGA01614F1
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                                                                                                                                                                                                 650-855-0572
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 74.0%;
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Pred. No. 51
                                                                                                                                                                                                                                             PF-0546 US
 Score 14.8;
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Length 605;
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RESULT 15
US-09-109-204-5
                                                                                                                                                                                        ; CLONE:
US-09-109-204-5
Search completed: September 7, 2002, 18:21:07 Job time: 28761 sec
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                                                                                                                      Matches
                                                                                                                                   Best Local Similarity
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Patterson, Chandra TITLE OF INVENTION: HUMAN TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2125 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                          LIBRARY: Dec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Hillman, Jennifer L.
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                                                                                                                                                                                                                                                         single
                                                                                                                                     74.0%;
88.9%;
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                                                                                                                                     Score 14.8; DB 3;
Pred. No. 67;
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Minimum DB seq length: 0 Maximum DB seq length: 2
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16.8
16.8
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1: /SIDS1/gcgdata/h
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1736436 segs, 858457221 residues
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1994 DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
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                        AAV39297
AAH51750
AAL03245
                                                                                                                  AAS51323
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AAC18125
                                                                                            AAT03501
                                                                                                                                                                                         AAZ88701
                                                                                                                                                                                                                                                                                                         SUMMARIES
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30.143 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignments)
                                                                                                                                                                                                                                          Description
                               Chromosome 13q31-q
Human reproductive
                                                                              Human secreted pro
Papilloma virus ma
Human RAD54 nuclei
                                                                                                                                                                     Human CD95 recepto
Enterococcus faeca
              Human reproductive
                                                                                                                                                  Enterococcus
                                                                                                                                                  faeca
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(1100	AATSSBOU	17	2019	77.0	15.4	45
a str	AAV32467	1 4	1920	77.0	15.4	44
••	HATOSCOS	L	ROFT	77.0	15.4	43
Gene for firefly 1	ט ט ע	, <u>_</u>	1704		15.4	42
۲	AAT 63268	18	1704	77.0	15.4	41
{ ; ;	AAX25/1/	20	1656	77.0	15.4	40
Firefly luciferase	AAX25718	20	1644	77.0		39
. Lacer	AAX84396	20	1644	77.0		38
	AAX84395	20	1644	77.0	15.4	37
Inermostable lucif	AAQ34745	14	1644		15.4	36
	AAQ03257	11	1644		15.4	w i
prosopnia meranog	AAH29252	22	496			3 6
Human Secreted Pro	AAC16954	21	150			ا در ا در
Human reproductive	AAL03473	22	32172		5	، ا د
Prosopritia meranos	ABL19384	23	16989		5	ا بد
Sount of the Control	ABL16462	23	6396		S	30
	ABL13428	23	4005			29
_	AAD07071	22	3627			28
Human Sirar-i yeno	AAZ49396	21	3627			27
Drosophila meranos	ABL16463	23	3123			26
Human cyclic nucle	AAD25729	24	2757			25
DNA elicouring nover	AAS69653	23	2516			24
Bactitus antituces	ABA90868	24	2108			23
-	ABL13429	23	2005	_		22
Human porymeteors	AAK51978	22	1294			21
	AAK52962	22	1229			20
	AAS91613	23	1227		15.8	19
	AAH93924	22	1195	9.0		9 1
prost	AAS64160	22	1195	9.0		17
	AAD07067	22	1193	9.0		16
	AAZ49395	21	1193	9.0		55
secreted	AAF63808	22	1157			14
Human EST derived	AAH99123	22	396	2.0		ا بد
Ö	AAH41226	22	149980	4.0		17
Human DAZ genomic	AAZ92583	21	43795	84.0	16.8	1 6
Enterococcus faeca	AAX13026	20	007	84.0	16.8	10

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## ALIGNMENTS

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AAZ88701
ID AAZ
RESULT
                                                                                                                                                                                                                                                                                          AAZ88701 standard; DNA; 20 BP
                                                                                                                                                                                                          p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                             Human CD95 receptor promoter DNA p53 binding fragment #1.
                                                                                                                                                                                                                                                    11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                       AAZ88701;
      Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy \dot{\ }
                                                        Krammer P, Mueller-Schilling M, Oren M;
                                                                                                                                         03-FEB-2000
                                                                                                                                                             DE19847779-C1
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                   cancer chemotherapy; ss.
                                     WPI; 2000-162245/15.
                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                  16-OCT-1998;
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RESULT 2
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Best Local
           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are precured to the stabhylococcus aureus, Salmonella typhi, Klebstella invention is also useful for the identification of potential new targets to identify proteins used in proliferation, to express these proteins, and the control of proteins used in proliferation, to express these proteins, and the control of proteins used in proliferation, to express these proteins, and the control of proteins used to identify proteins used in proliferation, to express these proteins, and the control of proteins used to identify proteins used in proliferation, to express these proteins, and the control of proteins used to identify proteins used in proliferation, to express these proteins.
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to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                Claim 27; Seq ID No 3905; 511pp; English.
                                                                                                                                                                                                           antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                           New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                     P-PSDB; AAU33464.
                                                                                                                                                                                                                                                                                                                                    Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                      Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; ds; prokaryotic cellular proliferation gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis DNA for cellular proliferation protein #100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibiotic; antibacterial; drug design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS51323,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor promoter which is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                                     2001-611495/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 5; 12pp; German.
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2000US-242578P.
2000US-253625P.
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2000US-206848P.
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                                                                                                                                                                                                                                                                                                                    Xu HH;
                                                                                                                                                                                                                                                                                                                                  Ohlsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                             Zyskind Jw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                             Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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.57;
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                                                                                                                                                                                                                 · of
                                                                                                                                                                                                                                                                                                                         Carr GJ;
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AAS53070,
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       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                           Claim 27; Seq ID No 6707; 511pp; English.
                                                                                                                                                                           antibiotics, comprise sequences of
                                                                                                                                                                                                                        P-PSDB; AAU35211.
                                                                                                                                                                                                                                                                                Haselbeck R,
                                                                                                                                                                                                                                                                  Yamamoto RT,
                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis DNA for cellular proliferation protein #498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; ds; prokaryotic cellular proliferation gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS53070 standard; DNA; 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in exsential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part for the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 234 BP; 84 A; 33 C; 46 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                     polynucleotides for the identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 AGAAATGCACAAACTGTTTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                     2001-611495/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
proteins used in proliferation, to express these
                                                                                                                                                                                                                                                                                                                                17 2000US-206848P.

17 2000US-207727P.

17 2000US-242578P.

17 2000US-253625P.

18 2000US-257931P.

19 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                 Xu HH;
                                                                                                                                                                                                                                                                                Ohlsen
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90.0%;
                                                                                                                                                                                                                                                                          Zyskind JW,
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Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                           antisense
                                                                                                                                                                                                                                                                          Wall D,
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                                                                                                                                                                        nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                  development of
                                                                                                                                                                                                                                                                        Trawick JD,
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                                                                                                                                                                        acids
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                                                                                                                                                                                                                                                                     Carr GJ;
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proteins,

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RESULT
AAC18125
Query Match
Best Local
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 306 BP; 117 A; 40 C; 65 G; 84 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC18125 standard; cDNA; 338 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein 5' EST, SEQ ID NO: 22200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC18125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                 mRNAs encoding secreted proteins. No ORF has yet, been conclusively man and secreted proteins. No ORF has yet, been conclusively man RNAs encoding secreted proteins. No ORF has yet, been conclusively man RNAs or polyA+ RNAs derived from 30 different tissues. EST total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J, Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 AGAAATGCACAAACTGTTTT 86
                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 22200; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                      expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; Ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%;
90.0%;
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Pred. No. 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giordano
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                                                                                                   Query Match
Best Local :
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 밁
                                                      Query Match
Best Local Similarity
                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 338 BP; 86 A; 60 C; 42 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT03501 standard; DNA; 661 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papilloma virus major capsid protein DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skin carcinomas; therapy; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HP-Virus 49; papilloma virus; major; capsid protein; plasmid VS40-7; DSM 9135; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papilloma virus.
                                                                                                                                                                                                                                                                                                                                                                04-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                             DE4415743-A1
                                                                                                                                 peptide of papilloma virus (PV) major capsid protein and is expressed by the plasmid VS40-7 (DSM 9135). The DNA is useful in diagnosis, esp. to detect PV in skin carcinomas. Major capsid proteins encoded by a PV genome contg. the DNA are useful for
                                                                                                                                                                                                                                                                                               de Villiers zur Hausen E,
                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                           04-MAY-1994;
                                                                                                                                                                               AAT03501 is 78.5% homologous to HP-Virus 49, encodes AAR88269 a
                                                                                                                                                                                                                                     DNA encoding peptide(s) of papilloma virus major capsid
                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                 Sequence 661 BP; 195 A; 118 C; 155 G; 193 T; 0 other;
                                                                                                                                                                                                      Claim 1; Fig 3; 15pp; German.
                                                                                                                                                                                                                             useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 agaaatggccaaactgtttt 38
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 567
                     1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                         1995-383680/50
AGAGTTGCCCAAAGTGTTTT 548
                                                                                                                                                                                                                           for detecting papilloma virus in skin carcinoma
                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR88269
                                                                                                                          and/or vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                             94DE-4415743
                                                                                                                                                                                                                                                                                                                                                                   94DE-4415743
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%;
90.0%;
                                                          84.0%;
                                                                                                                                                                                                                                                                                                Leigh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 4
                                                 0
                                                          Score 16.8; DB 16;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                 Mismatches
                                                                                                                                                                                                                                                                                                   Shamanin V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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                                                                                                                                                                                                                                                                                                     zur Hausen H;
                                                                       Length 661;
                                                     Indels
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                                                     Gaps
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AAV39297 RESULT

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RESULT
AAH51750/
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                                                                                                                                                                                                                                                                 The present sequence represents a specifically claimed partial nucleic acid sequence encoding human RAD54 (hRAD54). A method for analysing a CC sample for mutation of DNA encoding hRAD54 has been developed using a CC DNA sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present identified as one of four minimal regions of chromosome 1 deletion in CC alia, that have been identified as novel hRAD54 is useful for production of proteins, inter CC amino acid sequence given in AAW62186 and known amino acid sequences cc cancer, including Xeroderma Pigmentosum and Bloom syndrome, Werner's CC syndromes and X-linked mental retardation with alpha-thalassaemia CC detecting complementary nucleotides for use as a diagnostic agent, cc especially useful for diagnosis of disease or susceptibility to diseases. XXX proteins are useful in gene therapy.
 29-AUG-2001
                                                  AAH51750 standard; DNA; 3001 BP
                               AAH51750;
                                                                                                                                                                                                                                              Sequence 2008 BP; 489 A; 419 C; 570 G; 526 T; 4 other;
                                                                                                                       139 agagatgcccaaactgagtt 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 27-28; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human hRAD54 DNA and polypeptide - and agonists, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-274189/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome; werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP844305-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human RAD54 nucleic acid sequence comprising exons 5-8
                                                                                                                                                 1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV39297 standard; cDNA; 2008 BP
                                                                                                                                           Conservative
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(first entry)
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                                                                                                                                                                                             84.0%;
90.0%;
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                                                                                                                                                                               0;
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Pred. No. 5
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robbins DJ;
                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                      Length 2008;
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                                                                                                                                                                         Gaps
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427 AGAGCTGCCCAAACTGCTTT 408

l agagatgcccaaactgtttt 20

Matches Query Match

18;

Conservative

0;

Local

Similarity

84.0%; 90.0%;

Score 16.8; Pred. No. Mismatches 61;

DB 21; 2;

Length 3001; Indels

0;

Gaps

0,

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AAH51601 represents a human genomic nucleotide sequence comprising sbg1, CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the CC human chromosome 13g31-g33 locus. The nucleotide sequences contain CC hab62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and polymorphisms. Sequences AAH51602 - AAH51626 and CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018 CC cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used crpresented by sequences and protein products. Primers AAH51632 - AAH51699 are used CC amplicons which comprise biallelic markers located on the chromosome CC amplicons which comprise biallelic markers located on the chromosome CC are represented in the sequences by degenerate/undefined base codes. PCR CC grimers AAH51818 and AAH51819 are used in the isolation of sequences of CC the invention. The biallelic marker containing nucleotide sequences of used to determine the identity of the nucleotide at a biallelic marker in CC genotyping by determining the identity of a nucleotide at a Region CC subjects. By determining the frequency of a biallelic marker in a prodistory of a nucleotide at a Region can be predistored to determine a predisoposition to or early onset of schizophrenia or treatment against schizophrenia or bipolar disorder or a beneficial response to or side effects related to
Sequence 3001 BP; 842 A; 608 C; 584 G; 966 T; 1 other;
                                    treatment against schizophrenia or bipolar disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 643-644; 737pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides comprising sequences from sbg1 and g35018 biallelic markers are used for genotyping and detecting schizophrenia or bipolar disorder and predisposition to these disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-619082/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999;
30-APR-1999;
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29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000; 2000WO-IB00435
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biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromosome 13q31-q33 biallelic marker containing amplicon SEQ ID 162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0126903.
99US-0131971.
99US-0132065.
99US-0143928.
99US-0145915.
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99US-0146453.
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AACIO
T 8 245/c 24
5 standard; DNA; 9821 BP.  2001 (first entry)  reproductive system related antigen; reproductive system gene therepy; ds.  2001.  2001.  2001.  2001.  2000.
PR P
EP-2000; EP-200
2000US-0232397. 2000US-0232398. 2000US-0232400. 2000US-0233063. 2000US-0233063. 2000US-0233063. 2000US-0233063. 2000US-0233063. 2000US-0234273. 2000US-0234283. 2000US-0234283. 2000US-0234283. 2000US-0234283. 2000US-0236383. 2000US-0240960. 2000US-0241809. 2000US-0246478. 2000US-0246478. 2000US-0246478. 2000US-0246478. 2000US-0246478. 2000US-0246478. 2000US-0246528. 2000US-0246528. 2000US-0246528. 2000US-0246528. 2000US-0246511. 2000US-0246611. 2000US-0249211. 01. 2000US-0249211. 02. 2000US-0249211. 03. 2000US-0249211. 04. 2000US-0249211. 05. 2000US-0249211. 06. 2000US-0249211. 07. 2000US-0249211

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RESULT 9
AAL03246/c
ID AAL0322
XX AAL032
XX 21-NOV
DE Human
XX Human;
KW Cancer
XX Homo s
PN W02001
XX W2001
XX FPN W402001
XX FPN W402001
XX Homo s
PN W2001
XX Homo
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Best Local
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                            31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-AFR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human reproductive system related antigen DNA SEQ ID NO: 5934.
                                                                                                                                                                                                                                                                                                                                                                  WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL03246 standard; DNA; 9824 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL03246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2800 AGAGCTGCCCAAACTGCTTT 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 5933; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465570/50.
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mes 18; Conserv
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                        2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-018350.
2000US-0189874.
2000US-0190076.
2000US-0199123.
2000US-0205515.
2000US-020467.
2000US-0214886.
2000US-0214886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0251030.
; 2000US-0251988.
; 2000US-0256719.
; 2000US-0251479.
; 2000US-0251856.
; 2000US-0251868.
; 2000US-0251869.
; 2000US-0251989.
; 2000US-0251990.
; 2000US-0254097.
; 2000US-0254097.
; 2000US-0254097.
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Pred. No. 7/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 3341 T; 0 other;
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    22-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
30-AUG-2000
30-SEP-2000
01-SEP-2000
01-SEP-2000
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05-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
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14-SEP
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14-AUG-2000;
18-AUG-2000;
2000US-0239935.
2000US-0239937.
2000US-0240960.
2000US-0241221.
2000US-0241785.
2000US-0241787.
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2000US - 0234223
2000US - 0234274
2000US - 0234997
2000US - 02354998
2000US - 0235834
2000US - 0235834
2000US - 0235836
2000US - 0236367
2000US - 0236368
2000US - 0236368
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2000US - 0236368
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2000US-0232401.
2000US-0233063.
2000US-0233064.
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2000US-0232398.
2000US-0232399.
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2000US-0229345

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2000US-0229513

2000US-0230437

2000US-0231438

2000US-0231242

2000US-0231243

2000US-0231244

2000US-0231413

2000US-0231413
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2000US-0232081.
2000US-0231968.
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2000US-0237037.
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2000US-0237039.
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2000US-0216880.
2000US-0217496.
2000US-0217496.
2000US-0220964.
2000US-0224518.
2000US-0224519.
2000US-0225213.
2000US-0225214.
2000US-0225214.
2000US-0225267.
2000US-0225268.
2000US-02252681.
2000US-0225758.
2000US-02258681.
2000US-02258681.
2000US-0227009.
2000US-0229824.
2000US-0229824.
2000US-0229824.
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2800 AGAGCTGCCCAAACTGCTTT 2781

1 agagatgcccaaactgtttt 20

Query Match Best Local Similarity

84.0%;

Score 16.8; Pred. No. 74;

DB 22;

Length 9824; Indels

Matches

18;

Conservative

0;

Mismatches

N

0;

Gaps

0;

AAX13026 RESULT 10

AAX13026 standard; DNA; 20072 BP

AAX13026;

19-MAR-1999 (first entry)

Enterococcus faecalis; contig; detection; Enterococcal infection;

vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis

Enterococcus faecalis genome contig SEQ ID NO:89

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08-NOV-2000;
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17-NOV-2000;
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                                                                                              WPI; 2001-465570/50.
                                                                                                            Rosen CA,
                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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2000US-0246476.
2000US-0246477.
                                                                                                             Barash SC,
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2000US - 0249208.
2000US - 0249208.
2000US - 0249210.
2000US - 0249211.
2000US - 0249213.
2000US - 0249213.
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2000US-0250160.
2000US-0250391.
2000US-0251030.
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2000US-0246526.
2000US-0246527.
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2000US-0246613.
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2000US-0246532.
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                                                                                                                                         2001US-0259678
                                                                                                                                                        2000US-0251990.
                                                                                                                                                                                                   2000US-0251988
2000US-0256719
                                                                                                                                                                                                                                                                                   2000US-0249244
                                                                                                             Ruben SM;
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14-NOV-1997; 06-MAY-1997; 16-MAY-1997;

97US-0066009. 97US-0044031. 97US-0046655

Barash SC,

Dillon PJ,

Kunsch CA;

WPI; 1999-045171/04.

(HUMA-) HUMAN GENOME SCI INC

04-MAY-1998; 12-NOV-1998 WO9850555-A2.

98WO-US08985

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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
Sequence 9824 BP; 3057 A; 1735 C; 1689 G;
                                                                                                                                                  Disclosure; SEQ ID NO 5934; 1297pp + Sequence Listing; English.
                                                                                                                                                                                    in preventing, treating or ameliorating a medical condition
            3343 T; 0 other;
                                                                                                                                                                    Qy
                                                                                              Query Match
Best Local (
                                                                            Matches
                                                                                                                                                                                                                    A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based primary nucleotide sequences, also known as contigs. The computer-based of Enterococcus faecalis genome with system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and focuse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 596-606; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection.
                                                                                                                                                                  Sequence 20072 BP; 5846 A; 4288 C; 3266 G; 6628 T; 44 other;
                  1 agagatgcccaaactgtttt 20
                                                                              18;
                                                                                                Similarity
                                                                              Conservative
                                                                                                90.0%;
                                                                                  0;
                                                                                                    Pred. No.
                                                                                                                  Score 16.8;
                                                                                  Mismatches
                                                                                                                        DB
                                                                                                                        20;
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protein of the invention.

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7383 agaaatgcacaaactgtttt 7402

Length 20072;

0,

Gaps

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TX SX FX EX E
                                                                                                                                                         B
                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                               The invention relates to a family of human genes referred to as the CC DAZ gene family, and to a functional DAZ homologue, DAZH. Members of the CC DAX gene family are clustered in the same region of the Y chromosome. CC In particular, the invention relates to an isolated DAZ gene (AAZ9249) present in interval 6D and/or 6E of the distal portion of Yq, mutations (CC in which are associated with reduced sperm count. The DAZH gene CC family, including DAZH is expressed in germ cells. DAZ and DAZH cnucledide sequences may be used as a source of primers and probes for CC or deletion of the DAZ gene. They are also used as human chromosome Y reduced sperm count associated with alteration CC or deletion of the DAZ gene. They are also used as human chromosome Y reduced sperm counts. Sequence AAS9249 represents human DAZ cDNA, and CC aAZ92491-Z92492 are partial DNA sequences of DAZ gene family members.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ92583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                  22516 agagattgccaaactgtttt 22535
Pyrococcus abyssi genomic fragment #5
                                29-OCT-2001
                                                                               AAH41226 standard; DNA; 349980 BP
                                                             AAH41226;
                                                                                                                                                                                                                                                                Sequence 43795 BP; 12175 A; 8166 C; 8183 G; 15271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 11A-L; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid, useful for diagnosis and treatment of reduced sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-181393/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-1994;
31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6020476-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAZ gene; chromosome rq; male infertility; sperm count; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DAZ genomic sequence, SEQ ID NO:101.
                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ92583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ92583 standard; DNA; 43795 BP
                                                                                                                                                                1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                             18;
                                                                                                                                                                                                         Conservative
                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reeve MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0690734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0310429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0742185.
                                                                                                                                                                                                                    84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saxena R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                         0,
                                                                                                                                                                                                                    Score 16.8;
Pred. No. 9
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page DC,
                                                                                                                                                                                                                      95;
                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reijo R;
                                                                                                                                                                                                     2;
                                                                                                                                                                                                                             Length 43795;
                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                 Gaps
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XXX DXX AC
                                                                                                                                               AAH99123
                                                                                                                                                          RESULT
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FT
FT
FT
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Best Local Similarity
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                           53995 aaagatacccaaactgtttt 54014
              Human; sheep; pig; cow; fruit fly; yeast;
       tomato; monkey;
                                       Human EST-derived coding sequence SEQ ID NO: 980.
                                                                         12-OCT-2001
                                                                                                      AAH99123;
                                                                                                                          AAH99123 standard; cDNA; 396 BP
                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96042). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41225 and the 3' end of this sequence overlaps with the 5' end of AAH41227. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110
                                                                                                                                                                                                                                                                                                         Sequence 349980 BP; 98084 A; 80447 C; 77665 G; 93784 T; 0 other:
                                                                                                                                                                                                                                                                                                                                          AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 511-606; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleotide sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999;
                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR2792651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                         1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyperthermophilic archaeon; hyperthermophilic protein; ds.
                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                  Conservative
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thierry JC, Pri
Weissenbach J,
    dog; sea urchin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99FR-0005034.
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/*tag= b
/note= "This sequence overlaps with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..49980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "This sequence overlaps with the 3/
                                                                                                                                                                                                                                                             84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prieur D,
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                             Score 16.8;
Pred. No. 1
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                                                                                                                                                                                                                                               Mismatches
expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dietrich J,
                                                                                                                                                                                                                                                         1.3e+02
              hamster; macaque;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heilig R;
                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                      Length 349980;
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              horse;
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RESULT 1
AAF63808,
ID AAF6
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 396 BP; 80 A; 115 C; 86 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 766; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibodies and research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAM24464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                              Human; immunosuppressive; antiarthritic; antirheumatic; nootropic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cancer; cardiovascular disorder; cerebrovascular disorder; infection;
                                                                                                                                                                                                                                  03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                            AAF63808 standard; cDNA; 1157 BP
                           WO200077021-A1
                                                                                     secreted protein; ss.
                                                                                                   nervous system disorder; ocular disorder; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                   122 agaaatgcccaaactgtt 139
 21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               1 agagatgcccaaactgtt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-476164/51.
                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                      secreted protein gene 20 SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Liu C, Zh
Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ou P, Qian XB, Wang Z, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; | Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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which encode human secreted proteins AAB75280 - AAB75287. Included in the convention are protein sequences AAB75280 - AAB75287. Included in the convention are protein sequences AAB75280 - AAB75287. Included in the convention are protein sequences AAB75280 - AAB75287. Included in the convention are protein sequences AAB75280 - AAB75287. Included in the convention are protein sequences AAB75280 - AAB75287. Included in the convention are protein sequences with which these conventions and the activities of the activities of the proteins and conventions and the activities of their agonists and antagonists and antagonists and antagonists and antagonists and antagonists conventions; cerebroprotective; conventions and vulnerary activity. The protein and polynucleotide copthalmalogical; and vulnerary activity. The protein and polynucleotide sequences, their agonists and antagonists may be useful for treating, correcting and diagnosing diseases and disorders such as autoimmune conventing and diagnosing diseases and disorders such as autoimmune conventions are cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, c.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, c.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, c.g. corneal infection. The polypeptides can also be used to aid wound e.g. corneal infection. The polypeptides can also be used to aid wound e.g. corneal infection. The polypeptides can also be used to aid wound c.g. corneal infection. The polypeptides can also be used to aid wound e.g. corneal infection. The polypeptides can also be used to aid wound e.g. corneal infection. The polypeptides can also be used to aid wound c.g. corneal infection. The polypeptides can also be used to aid wound e.g. corneal infection. The polypeptides can also be used to aid wound to polypeptides can also be used as a food additive or preservative to c.g. corneal infections and contact trissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative t
                                                                                                                                                                                                                                                                          RESULT 15
AAZ49395/c
ID AAZ493
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
  KW KW XXX DXX AXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2000; 2000WO-US15135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 451; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing, treating or ameliorating preventing, treating or ameliorating preventing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1157 BP; 326 A; 223 C; 269 G; 339 T; 0 other;
                      Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response;
                                                                                                                                                                                         14-MAR-2000 (first entry)
                                                                                                                                                                                                                                     AAZ49395;
                                                                                                                                                                                                                                                                                  AAZ49395 standard; cDNA; 1193 BP
                                                                                                                                       Human STRAP-1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                               138 GAGAAGCCCAAACTGCTTT 120
cellular; humoral; anticancer vaccine; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 gagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-071257/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 22
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
            detection; diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CC (serpentine transmembrane antigen of the prostate). STRAP-1 is compensation transmembrane antigen of the prostate). STRAP-1 is compensation, but which show the prototype member of the STRAP family of proteins (AAY58194-Y88197) cc which exhibit a high degree of structural conservation, but which show cc gene has been localised to chromosome 792. STRAP-1 is thought to be a compensation of the stransmembrane protein and is expressed predominantly in prostate call protein characterised by six transmembrane domains and "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and corresponding to the stransmembrane at high levels and corresponding to extracellular and two intracellular loops. Throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is colon, compensate and ovarian cancer. The function of the STRAP protein is not compensate and ovarian cancer. The function of the STRAP proteins is not compensate and ovarian cancer. The function of the STRAP proteins is not compensate and covarian cancer that the presence of six transmembrane compensates. The structural immune stating bladder, colon, compensate and the protein induces cellular and humoral immune responses against compensation in the strapentic stating). STRAP-1 and compensate compensation and proteins are proteins may be used for detection, prognosis, compensation and proteins are proteins and be used for detection, prognosis, compensation and prognostic reagents, for identifying STRAP-expressing cells for screening linhibitors of STRAP expression. Since high levels of STRAP compensation and prognostic reagents, and because they are expressed mainly compensation of the cell surface, they are expressed mainly compensation of the cells, agents targetted to them should have the surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 1A; 83pp; English.
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P-PSDB; AAY58194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly for prostatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins useful as diagnostic markers and therapeutic targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Afar DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AFAR/) AFAR D E.
(HUBE/) HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SAFF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UROG-) UROGENESYS INC.
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drug targetting; recombinant protein; ds.
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) RAITANO A B.
SAFFRAN D C.
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98US-0091183.
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antigen of the prostate)"
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Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 other:

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                                            Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                              Matches
564 GAGAAGCCCAAACTGCTTT 546
          2 gagatgcccaaactgtttt 20
                                           Conservative
                                          0; Mismatches
                                                      Score 15.8; DB 21;
Pred. No. 1.7e+02;
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1.7e+02;
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Search completed: September 7, 2002, 18:39:44 Job time: 29878 sec

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and is derived by analysis of the total score distribution.
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1 (bases 1 to 20)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 12 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)
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Sequence 12 from Patent DE19847779.
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/db_xref="taxon:9606"
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AL591593 Zebrafish
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AC079160 Homo sapi
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Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 26 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)
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Sequence 26 from Patent DE19847779.
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 18 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Sequence 18 from Patent DE19847779,
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Mueller-Schilling, M., Krammer, P. and Oren, M.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2827)
                                                                                                                                     AX026092 2827 bp
Sequence 4 from Patent DE19847779
AX026092
                                                                     Homo sapiens
                                                                                        human.
                                                                                                                      AX026092.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-MAY-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND Overlaps with X81335, & X82279-X82286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rudert, F.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watson, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2344)
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complement(1237. .1244)
/note="lysozyme silencer 1"
1338. .1919
1920. .2344
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546 c 511 g
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Location/Qualifiers
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Sequence 1 from Patent DE19847779.
AX026089
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Novel receptor dna useful for identifying apoptosis-mounts are substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 1 03-FEB-2000;
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                                                                                                                                                                                                                          Human DNA sequence from clone
            Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Cione
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 187313)
                                                                                                                               Homo sapiens
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clonerequest@sanger.ac.uk
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During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em., EMBL; Sw:, Sw:, Sw: Sympore "re- "phrematic unit of the more than one manuscro".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping Group. Further information that it is a second with the formation of the formation in the formation of the formation of the formation in the formation of the formation 
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Direct Submission
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74951)
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/clone_lib="RPCI-11.2"
100119. .100156
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/db_xref="taxon:9606"
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100.0%; Pred. No. 2.2;
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Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:16944088.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with this sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em. EMBL; Sw:, Gatabases can be found at
                                   Homo sapiens chromosome 1 clone RP4-722L13 map p22.3-31.2, ***

AL365355
                                                                                                               AL365355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP11-480N10 1s from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                               Conservative
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a 14184 c 13984 g 21266 t
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/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone.Restriction digest data confirm the assembly."
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/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPCI-11.2"
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 87417 bases at least Q30 Consensus quality: 88119 bases at least Q20 Insert size: 89678; sum-of-contigs Insert size: 92914; 9.4% error; agarose-fp Quality coverage: 4.75x in Q20 bases; sum-of-contigs Quality coverage: 4.78x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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On Aug 12, 2000 this sequence version replaced gi:9187428.
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                                                                                                                                                                                                                                                                                                                                                                                               17236 17335: gap of 100 bp 10 length 17336 21293: contig of 3958 bp in length 21394 21393: contig of 3958 bp in length 21394 37557: contig of 16164 bp in length 37558 37657: gap of 100 bp 37658 54929: contig of 17272 bp in length 54930 55029: gap of 100 bp 55030 62839: contig of 7810 bp in length 62840 62939: gap of 100 bp 62840 674511: contig of 7810 bp in length 74612 83633: contig of 9022 bp in length 83634 83733: gap of 100 bp 83734 90478: contig of 6745 bp in length 83734 90478: contig of 6745 bp in length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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12490 17235: contig of 4746 bp in length
17236 1735; gap of 100 bp
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                    /note="assembly_fragment:00528
fragment_chain:1"
                                                                                                   /note="assembly_fragment:00957
fragment_chain:1"
                                                                                                                                                                                                                  /map="p22.3-31.2"
/clone="RP4-722L13"
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/db_xref="taxon:9606"
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                            Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 14, 2000 this sequence version replaced gi:7108032. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1108 2229: contig of 1122 bp in length
2230 2329: gap of 100 bp
2330 4120: contig of 1791 bp in length
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4221 6093: contig of 791 bp in length
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12757 19311; contig of 6555 bp in length
19312 19411; gap of 100 bp
19412 24024; contig of 4613 bp in length
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30617 30716: gap of 100 bp
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/clone="RP11-23I23"
/note="assembly_fragment"
                                                                                                                                                              /organism="Homo sapiens"
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123134; contig of 16995 bp in length
                                                                                                                                                                                                                                                                                                                                                                   727: gap of 100 bp
91285: contig of 12558 bp in length
1385: gap of 100 bp
1106039: contig of 14654 bp in length
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-1: gap of
78627:
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45340: contig of 9410 bp in length
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Best Local Similarity 95.0%;
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                               Direct Submission
Submitted (16-NOV-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Nov 16, 2001 this sequence version replaced gi:12331033.
                                                                                                                                                                                                                                                                        Homo sapiens chromosome 1 clone RP11-193H16, WORKING DRAFT SEQUENCE, 9 unordered pieces. AC099561 AL356153 AC099561.1 GI:16945998
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
                                                                                                                                                   Direct Submission
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    Center: University of Washington Genome Center
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31221 c 31549 g 49758 t
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123235. .140131
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56061. .67711
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30717. .35830
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12757. .19311
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; L08752; 90% of reads
Sequencing vector: plasmid; 10% of reads
Chemistry: Dye-terminator E1; 73% of reads
Chemistry: Dye-terminator B1g Dye; 27% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 176140 bases at least Q40
Consensus quality: 178264 bases at least Q30
Consensus quality: 179264 bases at least Q20
Insert size: 169266; 11.4% error; agarose-fp
Quality coverage: 8.9x in Q20 bases; sum-of-contigs
Quality coverage: 8.4x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Code: UWGC
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2456
/note="assembly_name:Contig106"
109809. .181497
/note="assembly_name:Contig107"
.34626 c 32770 g 55026 t
                                                                                                   /note≈"assembly_name:Contig105"
52282. .109708
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2456. .4495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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17171: contig of 4646 bp in length
17271: gap of unknown length
26889: contig of 9618 bp in length
26989: gap of unknown length
62181: contig of 35192 bp in length
62281: gap of unknown length
109708: contig of 47427 bp in length
109808: gap of unknown length
181497: contig of 71689 bp in length
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2455: gap of unknown length
4495: contig of 2040 bp in length
4595: gap of unknown length
7640: contig of 3045 bp in length
7740: gap of unknown length
12425: contig of 4685 bp in length
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  937 others
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Query Match Best Local S

Matches

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Db 75524 AGAAATGCCCAAACTGTTTT 75543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-NOV-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA on Feb 3, 2001 this sequence version replaced gi:11276152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 236685)

McCombie, W.R., Baker, J.P., Bahret, A., Bal, H., Balija, V.,

Dedhia, N.N., de la Bastide, M., Huang, E.N., King, L., Kirchoff, K.A.,

Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R.,

Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Toth, K., Vil, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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McCombie, W.R.
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                                                                                                                                                                                                                                                                                                                                                     Center clone name: RP23-15A13
                                                                                                                                                                                                                                                                                                                                                                                               Contact: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.cshl.org/genseq
                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: CSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory
                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence! It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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57894
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                 58002: gap of unknown length 72097: contig of 14095 bp in length 72206: gap of unknown length 85432: contig of 13256 bp in length 85541: gap of unknown length 98091: contig of 12550 bp in length 98200: gap of unknown length 110626: contig of 12426 bp in length 110735: gap of unknown length 110735: gap of unknown length 110983: contig of 9148 bp in length 119983: contig of 9148 bp in length
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             119883:
119991:
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                                                                           Db 236285 AGAAATGCCCAAACTGTTTT 236266
                    RESULT 13
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          AE001670
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                                                                                                                                Conservative
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/clone="RP23-15A13"
57976 c 57568 g 58324 t
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137470:
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191171: contig
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235387; contig of 1946 bp in length
235495; gap of unknown length
236685: contig of 1190 bp in length
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95.0%;
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Pred. No. 20;
             16157 bp
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                 BCT 01-DEC-2000
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Gaps

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TITLE JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

AUTHORS

SOURCE ORGANISM

VERSION

KEYWORDS ACCESSION RESULT 12 AC084744/c

DEFINITION

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
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 \mathtt{AE001670\ AE001363}
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YIGSEGLAIAMDRFGYSGASDDVSEECGFTTEQILQRILSQ"
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                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CPn0898"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVIAKLSSLGTTSLGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKIL
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                                 SOURCE
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      ORGANISM
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Chlamydophila pneumoniae AR39
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AE002255.2 GI:8163532
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MEGMISLFFWLCKVFCLGLALVAIIGTSNAVNLTDGLDGLAAGTMSFAALGFIFVALR
STIPIAODVAXYLAALYGACIGFLWYNGFPAOLFMGDTGSLLLGGLLGSCAVMLRAE
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/protein_id="Aab19039.1"
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/db_xref="GI:4377221"
/translation="MCORILIGIGITGKSVARELYQQGHYLIGADNSLESLISVDHL
/translation="MCORILIGIGITE THE NUMBER OF THE NUMBER
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/protein_id="AAD19038.1"
/db_xref="GI:4377220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFVCAGLGIAAVLWR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Muramidase (invasin repeat family)"
/protein_id="AAD19040.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11516. .1267:
/gene="ftsw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKARRLKPGDQLRIR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ftsW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.4;
Pred. No. 60;
                                                                                                                                                                                                                             17395 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16157;
                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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On Jun 1, 2000 this sequence version replaced gi:7189881.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHFQATTIGORFPKVVRSLGADSVCITGDFSLTAMDGEFLLAKHFVETLAKHSSVYLL
PGNHDVYTLKSLAQQTFYTHFPNDQLQQNKVSFHKITDHWWLILLDCSCLNGWFSANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="AAF38749.1"
/db_xref="GI:7189882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene=
118. .
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/strain="AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="conserved hypothetical protein; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVHLAQISAIETFLLSLSPEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKKYPKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CP0969"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: Chlamydia pneumoniae AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:115711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1030. .1251)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYLHGHEHQAAVYNCADTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MQEKPRHVHRIIHISDVHFHVLPVNPVHCFNKRLKGLLRKVFGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="conserved hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="meakkikelskeaqllkklreksrvldeknkrkawvaklvampe
SirelekeerveTpqlfqalaekileegv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
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                                                                                                                      /transl_table=11
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/translation="MYRRYSTSEFRYGLRIEIDGOPYLILQNDEVKPGKGQAFNRIKVK
                                                                                                                                                                                                                                                                                                               PID:536991; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                            complement(1295. .1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1295. .1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CP0971"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                 AKIMVPIFIDEGELVKVDTRTGSYESRVSK"
                                                                                         NFLTGRVIERTYKSGESVETADIVERSMRLLYTDQEGATFMDDETFEQEVVFWEKLEN
                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:U14003 SP:P33398 GB:X61676 PID:433670
                                                                                                                                                                                                                                                                                                                                                                              /gene="CP0971"
                                                        IROWLLEDTIYTLVLYNGDVVAVEPPIFMELSIAETAPGVRGDTASGRVLKPAVTNTG
                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                    NKHVDTGAGLERLVSLIAGTHTVFEADVLRELLAKTEQLSGKVYHPDDSGAAFRVIAD
HVRSLSFALAOGLLPGNTERGYVLRKILRRSVNYGRRLGFRNPFLAEIVPSLADANGE
AYPELKNSLSQIQKVLTLEESSFKTLDRGGNLLQQVLKSSSSSSCISGEDAFKLKDT
YGMPIDEISLLAKDYDYSVDMJTFHKLEQEAKERSKKNVVQSQGTSESITWELHLTSE
FIGYDHLSCDTFIEAIISKDHIVSSLOERQEGALVLKVSPFYAEKGQVGDSGEIFCS
EGTFIVTHTTSPKAGLLVHHGRISQGSLTVEAAVTAQVNRYRKRIANNHTACHLLHK
ALEITILGDHIRQAGSYVDDTKIRLDFTHPQAISPEDLLCIETLVNESIERNEPVDIRE
ALYSDVMNSSEIKQFFGDKYSDVRVVSAGHSHELCGGTHAEATGDIGFFRITKEHAV
NELENSLIQTKLDKLHINCHQRGITCLVHHLAEHENHRLQQYAQCLHQRIPEKLISL
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/note="similar to SP:P30958 GB:U00096 PID:1651547 PID:1651549 PID:1787357; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product "alany1-trna synthetase"
/product "alany1-trna synthetase"
/product "alany1-trna synthetase"
/product "alany1-trna synthetase"
/product "alany1-trna synthetase"
/db_xref="G1.7189887"
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AFAHEVSLSVFNENPEGIYATVHEKDDEAFALWEAYLPTDRIFRLTDKDNEWSM
ANTGPCGYCESLLFDRGPSFGNASSPLDDTDGERFLEYWNLVFMDENRTSEGSLLALD
ANTGPCGYCESLLFDRGPSFGNASSPLDDTDGERFLEYWNLVFMDENRTSEGSLLALD
ANTGPCGYCESLLFDRGFSFGNASSPLDDTDGERFLEYWNLVFMDENRTSEGSLLALD
                                                                                                                                /gene="CP0975"
7782. .11039
                                                                                                                                                                                                                             EVLNETLWQWISTQLI
                                                                                        /gene="CP0975"
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ETKOFWHLPEEKFEVPPAVKNFFAHKIQEDRKAQEQWLDEVRVWSKOFPELHEEFVAL
TSHKLPKNLESLVQSVEMPDSIAGRAASNKLIQVLVQHIPYLIGGSADLSSSDGTWIA
NEKVIHTYDFSGRNIKYGVREFGMATINMGLAYSQVFREFGGTELVFSDYMRNAIRL
ALSKLPVIYQFTHDSIFVGEDGPTHQPVEQLMSLRAIFGLYVIRPADANEVRGAWIAG
LKHTGPTVIVLSRAALPTLEAAHRPFEDGVGRGAYIVLKESGEKDDYTLFATGSEVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:J01581 SP:P00957 PID:145220 GB:J00096 PID:1789048; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALSVAKELEHLDKÖVRVVSFPCWELFEAQDVDYKOSIVGGDLGIRVSIEAGSALGWYK
YIGSEGLAIAMDRFGYSGASDDVSEECGFTTEQILQRILSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYLYGYVLRQNPRDPHWINRDRFVLSAGHGSXLLYSCLHLAGFDVSLEDLQEFRQLHS
RTPGHPEYGETYGVEATTGPLGQGLGNAVGMALSMKMLESRFNRPGHEIFNGKIYCLA
GDGCFMEGVSHEVCSFAGSLNLNNLVVIYDYNNVVLDGYLNEISVEDTKKRFEAYGWD
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THTTNIRFWEFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRK
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/gene="CP0973"
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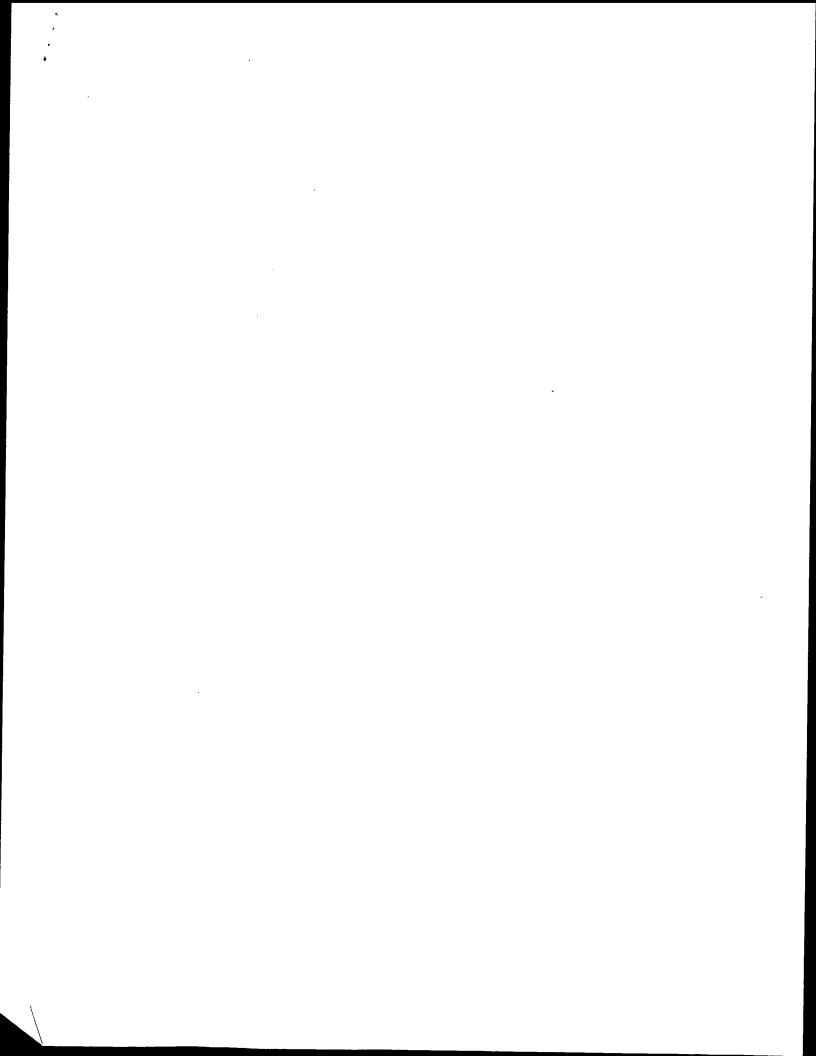
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VERSION
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Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                      Adams, M. and Venter, J.C. Direct Submission
                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 20563)
                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                  HTG; HTGS_PHASE2.
                                                                                                                                                                                                                            fruit fly.
                                                                                                                                                                                                                                                                          AC015202.1 GI:6436133
                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster,
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NPLLAFLQHLQEYMPPHGKPLKLAIYSTKTKSLKEARALAETVARGDVEIYERTGNLT
SSFALVNEAFAAISLSEFASTKVLRRQKQRTHESVTVEBYVVPIPGETVVHIHNGIGK
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IETGSMRIEFYQKIGNAESSEELTAIQEEMRDRFGFLPGEICWLFALAEIRLFALOHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSAFFDLLKSQTASHPPIWLLRQVGRYMPPYQELKGSQSLKTEF HNTEATVEATTLGPSLHVDAATLFADTLSILDGFAVITYDEAFGFRIOFSPEQPFTFT SDPQTIFSYLDAITLKGKLPVPLIVFAASPTLACYLIPEASKDFSKDFSKTYVY PEKFDQLISTIIEGTAIYLKTQMDAGAAAVQLFESSSLRLPSALFTRYVTEDRNELLYVY PEKFDQLISTIIEGTAIYLKTQMDAGAAAVQLFESSSLRLPSALFTRYVTEDRNELLA KLKEQALPVSLFCRCFEENFYTLQATQADTLHPDYHVDLHRIQKNLMLSLQGNLDPAI
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11050. .12039
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MLTSEKGEFSCRGGIVDIFPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGKVSKISI
SPAYTEEASGGNYSHSLLDYFSTPPLYLFDNLEILEDDFADISGTLSSLPDRFFSIGT
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94.7%;
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Pred. No. 60;
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                                                                                                                                                             Insecta;
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	Search completed: September 7, 2002, 18:21:55	Oy 1 agagatgcccaaactgttt 19 .	Query Match 87.0%; Score 17.4; DB 2; Length 20563; Best Local Similarity 94.7%; Pred. No. 62; Handle 1; Indels 0; Gaps 0; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	/organism="prosophila melanogaster" /db_xref="taxon:7227"  BASE COUNT 6416 a 4099 c 4148 g 5900 t   ORIGIN	This second the according to the accordi	ROCKVILLE, MU, USA  COMMENT This sequence was identified as CDM:10213741 by the submitter.  For further information on this sequence e-mail to fly@celera.com.  * NOTE: This is a 'working draft' sequence.
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AQ375699 RPCI11-15 AQ108019 CIT-HSP-2 AW903211 CM4-NN102 C17241 C17241 Clon C16982 C16982 Clon

AA350574 EST57929
AV694681 AV694681
AA362251 EST71725
AV692265 AV692265
AV692265 AV692265
AV692267 HS\_228\_A
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AQ420313 RPCI-11-1
B35593 HS-1029-A2-B36994 HS-1042-A2-B36994 HS-

B39893 HS-1050 B1-AW297626 UI-H-BW0-B10814 F18415-Sp6. AV743395 AV743395 AV743395 AV743395 AI244275 gj81b01.x AI469365 ti71c12.x AQ170644 HS\_2165\_A B95491 CIT-HSP-216

AI635956 tz28e11.x

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Minimum DB seq
Maximum DB seq
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Perfect score:
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 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                    Score
37.4
36.8
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42.4
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191.387 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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AG093829
AQ708262
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AG019885
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AQ890907
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AGG19885 Homo sapi
AGG19562 Homo sapi
AA279976 zt08e01.s
AQ033226 HS_2226_A
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AQ708262 HS_571_A
AQ240694 CIT-HSP-2
AA376998 EST89574
                                                    AQ498448 HS_5088_B
AQ054706 CIT-HSP-2
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AQ603697 HS_2126_A
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     AQ889826 HS_3100_A
AQ890907 HS_3100_A
AQ375661 RPCI11-15
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10310 row: p column: 06
High quality sequence stop: 708.
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BG256799 G77777
                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMV-SpORT6; Site_1: NotI;
/site_2: SalI; Cloned unidifrectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4479221"
/clone_lib="NIH_MGC_92"
             Note: this is a NIH_MGC Library.
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     Homo sapiens genomic DNA, 21q region, clone: B2289H10 genomic survey sequence.
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Homo sapiens genomic DNA, chromosome 21q

Published Only in DataBase (1999) In press

2 (bases 1 to 488)

Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,

Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (16-OCT-1999) to the DDBJ/EMBL/GenBank databases.

Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato

University, 1-15-1 Kitasato, Sagamihara 228-8555, Japan

(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:042-778-9923,
AG019562
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                                                                                                              Insert Length: 717 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 398.
                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 717 Std Error: 0.00
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                     ocation/Qualifiers
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/map="21g"
135 c 140 g 241 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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 Mismatches

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Local Similarity 64.2%;
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A2 D01_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2226 Col=2 Row±G, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith, Young,J., Zhao,S., Adams,M.D. and Receir,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ033226.1 GI:3285414
                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                          99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                   scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hood, L
                                                                                                                                                                               High quality sequence stop: 421.
                                                                                                                                                                                                     Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                          Sequence Tagged Connector Plate: 2226 row: G colu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." a 99 c 107 g 140 t
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/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                    /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                           ocation/Qualifiers

 Mismatches

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Pred. No. 0.096;
0; Mismatches 34;
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                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 ACTTCAAGACCTTGNGCAAGTTATTTAATGTTTNT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 actaaccatctttgccaatgttgcttaagcttttt 119
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180 AAAAGCCCAGACTTTGAAGCCAGACTGCTTAGGTTCAAATCCTGGCTCTGCCAGTTATTA 239
                                  6
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1 Similarity 63.2%;
60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-094G15.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-603-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes DNA, clone: PTB-094G15.F, genomic survey sequence AG093829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tracking errors.
                                                                                                                                                                                              /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/close_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                           /clone="PTB-094G15.F"
                                                                                                                                                                                                                                                                                                           /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                   32.5%; Score 39; DB : 63.2%; Pred. No. 0.3;
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                                                                             133 TGGCTCTGTTACTTATAAGCTCTGCAACCTCGGGCAGATTACCTAAGTCAGTTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                           67 tgactctgctatttattaactaaccatctttgccaatgttgcttaagctttttt 120
                                                                                                                                             73 ATGGAGGGACAGAGATGGTAAAACATGGTCTTGGAAGCCAGACCGTCTGGGTTTGAATCC 132
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                           7 aagggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcc 66
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        AQ240694
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ708262 530 bp DNA linear GSS 07-JUL
HS_5571_A1_F11_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1147 Col=21 Row-K, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ708262.1 GI:5417688
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="Plate=1147 Col=21 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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                                                                                                                                                                                                                                         32.3%;
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                                                                                                                                                                                                                                    Score 38.8; DB 12; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                        104 g
 691 bp
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   DNA
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linear
GSS 30-SEP-1998
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REFERENCE
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AUTHORS
                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 ATGCAGAATTAAAAGTATAGGCACTGGAGCCAGATTCACTCAGTTTTAAATGCAACTCTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                   70 CAATTTCTTAGATAAATGACTTTGTCCAAGTTTCTTAAGCTT 29
                                                                                                                                                                                                                                                                                                                                                                                                                           75 ctatttattaactaaccatctttgccaatgttgcttaagctt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 atggcatagaaagaagcaggaccttgggagcaagaatatctaagtttaattcctgactctg 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                     9
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 367)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                              367 bp mRNA linear EST 21-APR-1997 EST89574 Small intestine I Homo sapiens cDNA 5' end, mRNA sequence. AA376998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                           AA376998.1 GI:2029388
                                                                                                                                                                                                                                                                                                          AA376998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seg primer: M13-21 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Other_GSSs: CIT-HSP-2386K22.TR.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 691)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIT-HSP-2386K22.TF.1 CIT-HSP Homo sapiens genomic clone 2386K22,
DNA sequence.
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a 99 c
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/clone="2386K22"
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Pred. No. 0.58;
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                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                             EST 21-APR-1997
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COMMENT
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                                                                                                                                                              AUTHORS
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Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weldman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Bednarik,D.P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
, Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter, J.C.

Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                        AQ498448
HS_5088_B1_F12_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=664 Col=23 Row=L, DNA sequence.
                                                                                                                                1 (bases 1 to 437)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                   AQ498448
                                                                         Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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99380589
                                                 scanning the
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                    Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: small intestine; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI" a 58 c 64 g 134 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="ATCC (inhost):181474"
/db_xref="taxon:9606"
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                                                       human genome
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Pred. No. 0.79;
0; Mismatches 16;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AAAAGCCTGAACTTTAGAGTAAAAATACCTACGTTTAAGTCCTGGTTCTCCTCTATATTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 act 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTT-HSP-2343H11.TF CIT-HSP Homo sapiens genomic clone 2343H11, DNA
                                                                                                                                                                                                            Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ054706
                                                                                         Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                  Unpublished (1998)
Other_GSSs: CIT-HSP-2343H11.TR
                                                                                                                                                                                           Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 AQ054706.1 GI:3351312
              Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                              Building
                                                     9712 Medical Center Dr., Rockville,
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 a
                                                                          Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 1 others a 72 c 71 g 155 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11 Human Male BAC Library"
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1. .437
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74.6%;
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                                                                  MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 actaaccatctttgccaatgttgcttaagctttttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                  High
                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (Plate: 0400 row: K column: 14
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 686)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482390942 686 bp DNA linear GSS 13-DEC-20010400K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0400K14 R, DNA sequence.
AZ590942
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                                                                                                                                                           quality sequence stop: 686.
                                                                                                                                                                                                                                                                                                                                                   308,
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                                                                                                                                                                                                                                                                                                                             USA
/db_xref="taxon:10090"
/clone="UUGC1M0400K14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                          Location/Qualifiers
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
102 c 104 g 178 t
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/sex="Male"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                        Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 TATTAGGAGCAAGAAGCTGCTAGAAATTATGTCTAAATTCACTTCTTNATTCAGTTATTT 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                             High quality sequence stop: 482.
                                                                                           Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2126 row: C column: 9
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                         High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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482 bp DNA linear GSS 10-JUN-1991  
HS_2126_A1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2126 Col=9 Row=C, DNA sequence. AQ603697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 482)
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                                                                                                                                                                                                                                                         (206) 616-3618
(206) 616-3887
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                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.5%;
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Pred. No. 1.5;
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AG040377/c
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Local Similarity 61.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG040377.1 GI:16569102
GSS; GSS (genome survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG040377 640 bp DNA linear GSS 01-NOV-200 Pan troglodytes DNA, clone: PTB-017M07.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC end sequences of Library PTB
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troglodytes male lymphoblast DNA, clone lib:PTB Chimpanzee Male Library clone:PTB-017M07.F.
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/clone="Plate=2126 Col=9 Row=C"
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                                                                                                       /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
143 c 125 g 180 t
                                                                                                                                                            /clone="PTB-017M07.f"
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               Score 35.8; DB 12; Pred. No. 2.5;
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                                                                           559 AAGAACACAGCCTCTGGAACCAGATTGCCTGAGCTCAAATCCTGTGTCTGCCACTTATTG 500
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GCTGTGTAATCTGGGCAAAGTTACTTAGAATCTCT 465
                 actaaccatctttgccaatgttgcttaagcttttt 119
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HS_3100_A1_E01_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3100 Col=1 Row=I, DNA sequence.
AQ889826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
plate: 3100 row: I column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 719)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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Class: BAC ends
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Similarity 61.1%;
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Location/Qualifiers
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151 c 108 g 233 t 1 others
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/sex="male"
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/db_xref="taxon:9606"
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Copyright (c) 1993 - 2000 Compugen
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                  US-10-035-832-1262

US-10-027-632-281585

US-10-027-632-29548649

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US-10-027-632-4265

US-10-027-632-4265

US-10-027-632-4265

US-10-027-632-4265

US-10-027-632-265257

US-09-345-882-1

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US-10-027-632-152436

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US-10-027-632-152439

US-10-027-632-152439

US-10-027-632-152439
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4266, App
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281585,
129548,
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248649,
295053,
27014, A
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14451, A
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28.2	28.2	28.2	28.2	28.2	28.3	28.5	28.5	28.5	28.5	28.7	28.7	28.7	28.7	28.8	28.8	28.8		29.0	29.0
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sequence 30420, A			Sequence 190488,	Sequence 18552/,	Sequence 2//529,	Sequence 14994, A	Sequence 2/3, App	`		Sequence 1885, Ap	a a	Sequence 10224/,	Sequence 619, App	Sequence 323053,	Sequence 10146, A			Sequence 2144, Ap	

ALIGNMENTS

## CURRENT APPLICATION UNMBER: US/10/035,832 CURRENT FILING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 1613 SOFTWARE: Patentin version 3.1 SEQ ID NO 1262 LENGTH: 45121 US-10-027-632-281585/c Sequence 281585, Application US/10027632 GENERAL INFORMATION: APPLICANT: Wang, David G. ITILE OF INVENTION: Identification and Mapping of Single Nucleotide ITILE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR APPLICATION NUMBER: US 60/218,006 Sequence 1262, Application US/10035832 GENERAL INFORMATION: APPLICANT: MORTLS, David APPLICANT: MORPHAND, Eric TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: A-71249/RMS/DCF FILE REFERENCE: A-71249/RMS/DCF ) ORGANISM: Homo sapiens US-10-035-832-1262 US-10-035-832-1262 RESULT δÃ В Matches 120; Conservative Query Match Best Local Similarity TYPE: DNA 100.0%; Score 120; DB 6; 100.0%; Pred. No. 2.7e-26; Mismatches 0; Length 45121; Indels 0;

Gaps

APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/198,676

FILING DATE:

2000-04-20

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SEQ ID NO 129548
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                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR EILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR ETLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                 TYPE: DNA
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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23 gaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatttat 82
                                                                                  Local Similarity
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                                                                          Score 36.4; DB Pred. No. 0.25;
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                                                            Mismatches
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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US-10-027-632-248649
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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LENGTH: 637
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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Local Similarity 59.0%;
les 62; Conservation
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FILING DATE: 1999-11-23
                      APPLICATION NUMBER: US 60/167,363
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US-10-027-632-295053
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; ORGANISM: Human
US-10-027-632-57014
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RESULT
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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LENGTH: 471
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 57014
LENGTH: 595
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 AAGAGCATGAACTCTGAAGCCAGACTGTCTATGTCTGAATCCCAACTTCATTGCTTACTA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 GCTACATGACCTTGGACAAATTACTTAACCTCTCT 222
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                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-4265
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Cramance 4265, Application US/10027632
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4265
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Best Local 9
                    SEQ ID
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR EILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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                                           PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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                                                                                                                   PRIOR APPLICATION NUMBER: US 60/146,002
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APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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TH: 604
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Pred. No. 0.34;
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US-10-027-632-265257
Sequence 265257, Application US/10027632
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US-10-125-540-595/c
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; ORGANISM: Human
US-10-027-632-4266
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Matches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 595
LENGTH: 13046
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ14C1
                    PRIOR
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ORGANISM: Homo sapiens
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                                                                                                       APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29
               APPLICATION NUMBER: US 60/156,358
FILING DATE:
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Pred. No. 0.7;
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows V.
SEQ ID NO 265257
LENGTH: 657
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BOUGUETET, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patent.pm
SEQ ID NO 1
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PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
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CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
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LOCATION: 99098
OTHER INFORMATION:
                                                           LOCATION: 97152
OTHER INFORMATION:
                                                                                                                                      FEATURE:
NAME/KEY: allele
LOCATION: 97122
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele LOCATION: 72794 OTHER INFORMATION:
                  NAME/KEY: allele
LOCATION: 99098
                                                                            NAME/KEY: allele LOCATION: 97152
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LOCATION: 93714
OTHER INFORMATION:
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LOCATION: 90842
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   5-130-257
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Pred. No. 0.4;
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NAME/KEY: allele LOCATION: 9081990865	NAME/KEY: allele LOCATION: 8805088096 OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52	NAME/KEY: allele NAME/KEY: allele LOCATION: 8805088096 OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31 FEATURE:	NAME/KEY: allele LOCATION: 7277172817 OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51 FEATURE.	NAME/KDY: allele LOCATION: 7277172817 OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30 FEATURE:	NAME/KBY: allele LOCATION: 160031 OTHER INFORMATION: 5-148-352 : polymorphic base G or T	NAME/KEY: allele LOCATION: 150329 OTHER INFORMATION: 5-145-24 : polymorphic base   A or G FEATURE:	NAME/KEY: allele LOCATION: 146345 OTHER INFORMATION: 5-143-101 : polymorphic base A or C	NAME/KEY: allele NAME/KEY: allele LOCATION: 146328 OTHER INFORMATION: 5-143-84 : polymorphic base   A or G	NAME/KEY: allele LOCATION: 134374 OTHER: INFORMATION: 5-140-361 : polymorphic base insertion of CA FEATURE:	NAME/KEY: allele NAME/KEY: allele LOCATION: 134362 OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A FEATURE:	NAME/KEY: allele LOCATION: 134134 COTHER INFORMATION: 5-140-120 : polymorphic base C or T	NAME/KEY: allele LOCATION: 108471 LOCATION: 108471 OTHER INFORMATION: 5-136-174 : polymorphic base C or T	NAME/KEY: allele LOCATION: 108308 COTHER INFORMATION: 5-135-357 : polymorphic base A or G	NAME/KEY: allele LOCATION: 108149 OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT FEATURE:	NAME/KEY: allele LOCATION: 108106 OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A	NAME/KEY: allele LOCATION: 106940 OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A	NAME/KEY: allele LOCATION: 103806 OTHER INFORMATION: 5-131-395 : polymorphic base A or T	OTHER INFORMATION: 5-130-276 : polymorphic base, A or G FEATURE:
COTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39		. EC	. E.	<u>2</u>	. F.	ä	TION: RE: JRE:	LOCATION: 9909499140 OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35 FEATURE: NAME/KEY: allele	E	B	. g		. E.	; LOCATION: 9709997145 ; LOCATION: 9709997145 ; OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50 ; FEATURE: ; AAME KEY: allele	Ó	0	; LOCATION: 9081990865 ; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70 ; FEATURE: ; NAME/KEY: allele	; FEATURE: NAME/KEY: allele

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RESULT 12
US-09-345-882-1
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APPLICANT: Bouguele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BOUGUELERET, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
           OTHER INFORMATION:
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LOCATION: 90842
OTHER INFORMATION:
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                          NAME/KEY: allele
LOCATION: 99117
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LOCATION: 99098
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LOCATION: 97122
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FEATURE:
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LOCATION: 93714
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LOCATION: 88073
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TYPE: DNA
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NAME/KEY: allele
LOCATION: 108127
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NAME/KEY: allele
                   LOCATION: 90819..90
OTHER INFORMATION:
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LOCATION: 72771..72817
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LOCATION:
NAME/KEY: allele
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LOCATION: 88050..88096
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LOCATION: 160031
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LOCATION: 146345
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LOCATION: 146328
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LOCATION: 134374
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LOCATION: 108308
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LOCATION: 93690..93
OTHER INFORMATION:
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LOCATION: 103783...
OTHER INFORMATION:
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LOCATION: 99094..99
OTHER INFORMATION:
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LOCATION: 99075..99121
OTHER INFORMATION: pol
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NAME/KEY: allele
LOCATION: 97130..97177
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LOCATION: 97099..97145
OTHER INFORMATION: pol
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OTHER INFORMATION:
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OTHER INFORMATION: complement polymorphic fragment 99-1437-325
NAME/KEY:
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OTHER INFORMATION:
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LOCATION: 103783..103828
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LOCATION: 97130..97177
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LOCATION: 97099..97145
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LOCATION: 93690.
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LOCATION: 106918..106966
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LOCATION: 99094..99140
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Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BOUGUELETET, LYdie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: 44.US5.DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/126,704
CURRENT FILING DATE: 2002-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 88073
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OTHER INFORMATION:
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            NAME/KEY: allele LOCATION: 103806
                                                  LOCATION: 99117
OTHER INFORMATION:
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                                                                 NAME/KEY: allele
LOCATION: 99117
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FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5
                    NAME/KEY: allele
LOCATION: 90819..90865
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LOCATION: 90819..90865
OTHER INFORMATION: com
FEATURE:
          OTHER INFORMATION:
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LOCATION: 88050..88096
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LOCATION: 72771..72817
OTHER INFORMATION: pol:
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LOCATION: 146328
OTHER INFORMATION:
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LOCATION: 72771..72817
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LOCATION: 160031
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LOCATION: 134374
OTHER INFORMATION:
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OCATION: 146345
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LOCATION: 134362
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LOCATION: 134134
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LOCATION: 108149
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LOCATION: 108106
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LOCATION: 106918..1 OTHER INFORMATION: FEATURE:
              OTHER INFORMATION:
                              NAME/KEY: allele
LOCATION: 108127..108177
                                                                  FEATURE
                                                                                LOCATION: 108127..108177
OTHER INFORMATION: polym
                                                                                                                                                                 NAME/KEY: allele
LOCATION: 108084..108130
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LOCATION: 108084..108130
OTHER INFORMATION: polymo
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LOCATION: 106918..106966
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LOCATION: 106918..106966
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LOCATION: 103783..103828
FEATURE
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LOCATION: 103783..103828
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OTHER INFORMATION: polymorphic
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic
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LOCATION: 99075..99121
OTHER INFORMATION: pol-
FEATURE:
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LOCATION: 97130..97
OTHER INFORMATION:
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LOCATION: 99094..99140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 97130..97 OTHER INFORMATION:
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LOCATION: 93690..93736
OTHER INFORMATION: pol
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LOCATION: 97099..97145
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LOCATION: 93690..
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            polymorphic fragment 5-135-198 SEQ ID60
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US-10-027-632-231146, Application US/10027632

Sequence 231146, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231146
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           Sequence 14, Application US/09984827

GENERAL INFORMATION:
APPLICANT: DEMEFILE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
FILE REFERENCE: 03806.0522-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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CURRENT APPLICATION NUMBER: US/09/984,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR TLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                      560 getetattaetttotaaetetgtgaetttgggeaaatgaettaa ,603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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57; Conserv
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58.7%;
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Pred. No. 1.7;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.2; DB 7; Pred. No. 0.52;
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                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Homo sapiens US-09-984-827-14
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SEQ ID NO 14
LENGTH: 7379
                                                                                                               Matches
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
1436 gaccttgggcaagctgcttagtctctct 1463
                                                       1376 gggagtttggagcatacagagctcaagttgaatcctgactttgctacttattggctatat 1435
                55;
                                                                                                               Conservative
                                                                                                                          29.3%;
                                                                                                               0;
                                                                                                                         Score 35.2; DB 5;
Pred. No. 0.94;
                                                                                                               Mismatches
                                                                                                               33;
                                                                                                                                        Length 7379;
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Search completed: September 8, 2002, 01:09:44 Job time: 37062 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/pna/US080_COMB.seq:*
/cgn2_6/ptodata/2/pna/US081_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2 US-09-573-080A-99 8 US-09-428-151A-2422 3 US-09-614-387-1897 2 US-60-230-445-917 9 US-60-206-020-98 3 US-60-242-679-316 0 US-60-213-177-302	US U	US-09-83 US-09-93 US-00-94 US-60-24 US-09-92 US-09-92 US-09-92 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72 US-09-72	17
Sequence 2422, App Sequence 1897, App Sequence 917, App Sequence 98, Appl Sequence 316, App Sequence 302, App	15, 85, 1053 1053 1053 239, 239, 239, 239, 145,	4, 2 1, 2 10, 2 9, 2 101, 101, 101, 101, 101, 101, 101, 101	Description

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; ORGANISM: Homo Sapiens
US-09-834-291-4
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                                                                                                                                            Sequence 1, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller Schilling, Martina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 0 0 0
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
        CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: PCT/DE99/03343 PRIOR FILING DATE: 1999-10-18 PRIOR APPLICATION NUMBER: DE 198 47 779.1 PRIOR FILING DATE: 1998-10-16 NUMBER OF SEQ ID NOS: 32
                                                                                                         APPLICANT: Oren, Moshe TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122
                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2827
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                                                                                                                                                                                                                                                                    61 aatteetgaetetgetatttattaaetaaeceatetttgeeaatgttgettaagetttttt 120
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12 US-60-233-937-211
12 US-60-233-937-211
12 US-60-233-937-211
10 US-09-764-874-8121
11 US-10-092-400-8123
11 US-10-092-400-8123
11 US-10-092-400-8123
11 US-10-092-400-8123
11 US-10-092-400-8123
12 US-60-245-228-209
14 US-60-245-228-29
15 US-60-238-272-83
12 US-60-238-238-5424
13 US-60-238-084-23
14 US-09-637-889-5424
15 US-60-208-596-27
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Pred. No. 1.9e-26;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                             Length 2827;
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Sequence 211, App
Sequence 8121, App
Sequence 8121, App
Sequence 8123, App
Sequence 8123, App
Sequence 8123, App
Sequence 209, App
Sequence 209, App
Sequence 2424, App
Sequence 281585,
Sequence 281585,
Sequence 23, Appl
Sequence 23, Appl
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Sequence 211,
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US-09-997-722-10
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Best Local S
Matches 120
                                                                                                                                                                                                                                                        Sequence 9, Application US/60245224 GENERAL INFORMATION:
                                                         SOFTWARE:
SEQ ID NO 9
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Best Local Sin
Matches 120;
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LENGTH: 3212
                                                                                            CURRENT APPLICATION NUMBER: US/60/245,224
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 177
                                                                                                                                                     APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR EILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR EILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
ORGANISM: HUMAN
                    TYPE: DNA
                                    LENGTH: 17974
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                                                                         FastSEQ for Windows Version 4.0
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Pred. No. 1.9e-26;
); Mismatches 0;
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                                                                                                                                                                                                                                                                           Sequence 10171, Application US/09922340 GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
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TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/353,690
CURRENT FILING DATE: 1999-07-14
CURRENT FILING DATE: 1999-07-14
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: US 09/217,517
EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: US 09/004,182
EARLIER FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
                                                            TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/922,340
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/353,690
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14562 ATGTGGTAGAAAGCACATAAACTCTGGCGCCAGACAAACTAAGGTCAAATCCTGATTTTG 14503
                                           NUMBER OF SEQ ID NOS:
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LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 TGGAGGAAAATGAAAGGCAATATCGAGAGCCTGGGCTCTGGCATCAGAATGCCTGAGTTC 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 taggggaaggggtatggcatagaaagagcaaggaccttgggagcaagaatatctaagttt 60
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Pred. No. 0.0034;
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Pred. No. 0.0071;
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FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(443)

OTHER INFORMATION: n = A,T,C or G

US-09-922-340-10171
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                                              RESULT 8
US-09-726-803-609
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 10171
LENGTH: 443
Sequence 609, Application US/09726803 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 09/217,517
PRIOR FILING DATE: 1998-12-22
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CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/353,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 TGGAGGAAAATGAAAGGCAATATCGAGAGCCTGGGCTCTGGCATCAGAATGCCTGAGTTC 87
                                                                                                                                                                                                                                  146 TGGAGGAAAATGAAAGGCAATATCGAGAGCCTGGGCTCTGGCATCAGAATGCCTGAGTTC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AAACCCTGTCTCTGCTTTTTGGTAACTGTGTGACTTTTGGGCCAAGTCCCTTAACCTCTCTT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aattootgactotgotatttattaactaaccatotttgocaatgttgottaagctttttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 taggggaagggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagttt 60
                                                                                                                                                                                   61 aatteetgaetetgetatttattaaetaaecatetttgeeaatgttgettaagettttt 120
                                                                                                                                         86 AAACCCTGTCTCTGCTTTTTGGTAACTGTGTGACTTTGGGCAAGTCCCCTTAACCTCTCTT 27
                                                                                                                                                                                                                                                               1 taggggaagggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagttt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Conservative
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%;
                                                                                                                                                                                                                                                                                                                                                       36.0%;
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                                                                                                                                                                                                                                                                                                                                                       Score 43.2; DB 34; Pred. No. 0.0071;
                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
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                                                                                                                                                                                                                                                                                                                                                                                Length 443;
                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICANT:
APPLICANT:
APPLICANT:

Gearing, David P.

TITLE OF INVENTION:

Holtzman, Douglas A. Kingsbury, Gillian A. NYENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

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US-60-205-418-135; Sequence 135, Application US/60205418; GENERAL INFORMATION:
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                                                                          RESULT
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; LOCATION: (1)...(518)
; OTHER INFORMATION: n = A,T,C or
US-09-726-803-609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-726-803-1202
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Fas
SEQ ID NO 1202
LENGTH: 684
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1202, Application US/09726803 GENERAL INFORMATION:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION.
FILE REFERENCE: 1600.2050-001
CURRENT APPLICATION NUMBER: US/09/726,803
CURRENT FILING DATE: 2000-11-30
CURRENT FILING DATE: 60/168,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2050-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 609
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CURRENT APPLICATION NUMBER: US/09/726,803
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,085
PRIOR FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                   586 agtcatgtggccttggtcatgttacttaacctttct 621
                                                                                                                                                                                     526 aaggagcatggactttgcagctagactgcctagtttagaatcctggctctgccatgtatt 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 agtcatgtggccttggtcatgttacttaacctttct 484
                                                                                                                                       84 aactaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                            389 aaggagcatggactttgcagctagactgcctagtttagaatcctggctctgccatgtatt 448
                                                                                                                                                                                                                                                                                  Match 36.0%;
Local Similarity 65.6%;
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                                                                                                                                                                                                                                                                     63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 4.0
Beasley, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                     Conservative
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65.6%;
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 Mismatches

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Pred. No. 0.0075;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                Score 43.2; DB 2
Pred. No. 0.0081;
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                                                                                                                                                                                                                                                                33; Indels
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US-60-207-583-151/c

Sequence 151, Application US/60207583

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: INCLETE ACID MOLITITLE OF INVENTION: AND USES THEREOF

Ellen ISCLATED HUMAN TRANSPORTER PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND USES THEREOF δÃ

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; SOFTWARE: FASTSEC; SEQ ID NO 135; LENGTH: 11532; TYPE: DNA; ORGANISM: HUMAN US-60-205-418-135
               Вb
                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-824-559-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1994, Application US/09824559
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Jakubowski, Joseph A.
APPLICANT: Jakubowski, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-559-1994
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                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1994
LENGTH: 396
                                                                                                Matches
                                                                                                                                                                                                                                                                                                              TILLE OF INVENTION: THEREFOR THE REFERENCE: 1600.2077-001
CURRENT APPLICATION NUMBER: US/09/824,559
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/193,437
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9929
SOFTWARE: Factor 6.
                                                                                                                                       Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/205,418
CURRENT FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 536
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLO
                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6451 tggaggaaaatgaaaggcaatatcgagagcctgggctctggcatcagaatgcctgagttc 6510
151 aagagcgtgaagttgggaaacagactgtctgaatttaaatcctaactctaccacttatta 210
                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 aattootgactotgotatttattaactaaccatotttgocaatgttgottaagctttttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 taggggaaggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagttt 60
                                                                                                62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
                                                                                              Conservative
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                                                                                                               35.7%;
66.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%;
                                                                                            0;
                                                                                     Score 42.8; DB 31; Length 396; Pred. No. 0.0092; 0; Mismatches 32; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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US-09-972-546-15

; Sequence 15, Application US/09972546

; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Beasley, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/207,583
CURRENT FILING DATE: 2000-05-30
               APPLICANT: STRITTMATTER, STEPHEN M. APPLICANT: CATE, RICHARD L. APPLICANT: SAH, DINAH W.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 32
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/60/230,445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: HUMAN FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: NAME/KEY: misc_feature LOCATION: (1)...(32768)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1184 GCTCTGTTACTTATAAGCTCTGCAACCTCGGGCAGATTACCTAAGTCAGTTT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1244 GAGGGACAGAGATGGTAAAAACATGGACTTGGAAGCCAGACCGTCTGGGTTTGAATCCTG 1185
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                                                                                                                                                                                       1184 GCTCTGTTACTTATAAGCTCTGCAACCTCGGGCAGATTACCTAAGTCAGTTT 1133
                                                                                                                                                                                                                                                                1244 GAGGGACAGAGATGGTAAAAACATGGACTTGGAAGCCAGACCGTCTGGGTTTGAATCCTG 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 actctgctatttattaactaaccatctttgccaatgttgcttaagctttttt 120
                                                                                                                                                                                                           69 actctgctatttattaactaaccatctttgccaatgttgcttaagctttttt 120
                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                     9 ggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctg 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32768
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                                                                                                                                                                                                                                                                                                                                      1 Similarity
68; Conserv
INVENTION: NOGO RECEPTOR HOMOLOGS
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                                                                                                                                                                                                                                                                                                                                                        34.7%;
60.7%;
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; NAME/KEY: modified_base; CONTION: (111030)..(111129); OTHER INFORMATION: a, t, c, US-09-972-546-15
RESULT 15
US-60-212-358-85
                                                                                                                                  Db 110804 gagggacagagatggtaaaaacatggacttggaagccagaccgtctgggtttgaatcctg
                                                                 Db 110864 gctctgttacttataagctctgcaacctcgggcagattacctaagtcagttt 110915
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                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                       Matches
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PRIOR APPLICATION NUMBER: 60/238,361
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: A116US
CURRENT APPLICATION NUMBER: US/09/972,546
CURRENT FILING DATE: 2001-10-06
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OTHER INFORMATION: a, t, c, (
NAME/KEY: modified_base
LOCATION: (111030)...(111129)
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t, c,
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Sequence 85,

Application US/60212358

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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     pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
     US-08-206-176-5
US-08-766-858A-4
US-07-797-556-1
US-08-308-881-1
US-09-058-263-1
US-09-058-264-1
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US-09-058-264-1
US-09-058-264-1
US-08-795-473B-4
US-08-795-473B-4
US-08-783-360A-4
US-08-987-743-16
US-08-987-743-16
US-08-987-743-7-3
US-07-928-464-4
PCT-US93-07347-4
US-07-928-464-5
US-07-928-464-5
US-07-928-464-6
PCT-US93-07347-3
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| 23.3 6312 1 1 23.3 6312 1 1 23.3 6312 1 1 23.3 6312 1 1 23.2 1679 1 1 23.2 1679 2 1 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 2 23.2 1679 3 23.2 1679 3 23.2 1679 5 22.7 2160 5 4 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 2160 5 22.7 | Se Se                                                   |            |                   |                  |                 |        |         |                 |                 |               |                 |                 |                 |                  |                 |                                              |             |              |              |
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| 1 US-08-261-432-3<br>1 US-08-261-432-5<br>1 US-08-261-432-6<br>1 US-08-261-432-7<br>1 US-08-201-256-6<br>1 US-08-701-265-5<br>1 US-08-701-265-5<br>2 US-08-805-478-5<br>2 US-08-801-238-5<br>2 US-08-801-238-5<br>2 US-08-801-228-5<br>3 US-09-104-296-5<br>5 PCT-US94-06380-3<br>4 US-09-213-817-3<br>4 US-09-213-817-3<br>4 US-09-27-38-498-30<br>5 PCT-US94-01624-30<br>ALIGNMENTS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | tion US,<br>N:<br>er, Ian                               |            | 2160              | 3160             | 59065           | 1679   | 1679    | 1679            | 1679            | 1679          | 1679            | 1679            | 1679            | 1679             | 1679            | 6312                                         | 6312        | 6312         | 6312         |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 206176<br>Rael A                                        | ALIGNMENTS | PCT-US94-01624-30 | US-09-273-839A-7 | US-09-813-817-3 | 06380- | -09-104 | US-08-801-228-5 | US-08-801-238-5 | -08-802-627A- | US-08-805-478-5 | US-08-284-586-5 | US-08-701-265-5 | US-08-076-093A-5 | US-08-202-056-6 | -08-261-432-                                 | 08-261-432- | -08-261-432- | -08-261-432- |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                         |            | 30,               | _                |                 |        |         |                 |                 |               |                 |                 |                 |                  |                 |                                              | -           |              |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                         |            | Appl              | Laay<br>Laay     | Appli           | Appli  | Appli   | Appli           | Appli           | Appli         | Appli           | Appli           | Appli           | Appli            | Appli           | Appli                                        | Appli       | Appli        | Appli        |

## TELEPHONE: 206-547-8080 e: TELEFAX: 206-548-2329 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 10564 base pairs APPLICANT: DAILYMPIE, MICHAE APPLICANT: Prunkard, Donna E APPLICANT: Foster, Donald C TITLE OF INVENTION: Producti TITLE OF INVENTION: Animals COMPUTER READABLE FORM: MEDIUM TYPE: Floppy REFERENCE/DOCKET NUMBER: 93-15 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-547-8080 ext 322 ATTORNEY/AGENT INFORMATION: NAME: Parker, Gary E REGISTRATION NUMBER: 31-CORRESPONDENCE ADDRESS: FEATURE: IMMEDIATE SOURCE: CLONE: human fibrinogen gamma chain CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: MOLECULE TYPE: NAME/KEY: LOCATION: LOCATION: LOCATION: APPLICATION NUMBER: US/08/206,176 FILING DATE: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CITY: Seattle STATE: WA CLASSIFICATION: 435 ADDRESSEE: ZymoGenetics, Inc. STREET: 4225 Roosevelt Way, N.E. TYPE: nucleic acid TOPOLOGY: STRANDEDNESS: 98105 USA join(1799..1876, 1973..2017, 2207..2390, 2510 ..2603, 4211..4341, 4645..4778, 5758..5942, 7426 ..7703, 9342..9571) linear DNA (genomic) double Production of Fibrinogen in Transgenic 31-648 Ħ

US-08-206-176-5

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  ATTORNEY/AGENT INFORMATION: NAME: Crook, Wannell M.
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,858A
FILING DATE: 13-DEC-1996
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 13-FEB-1996
  COMPUTER READABLE FORM:
  APPLICANT: Hickey, Erin K.
APPLICANT: O'Connell, William A.
TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING
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  ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,1
REFERENCE/DOCKET NUMBER:
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19911122
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
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  TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
   FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
   SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
  APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
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   NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
   FILING DATE: 1:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
   FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese Kathryn A.
REGISTRATION NUMBER: 32.172
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
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LENGTH: 2369 base pairs
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  Sequence 1, Application US/09059099 Patent No. 5925740
  GENERAL INFORMATION:
APPLICANT: MOSSLEY, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
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  TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
  SOFTWARE: Microsoft Word, Version 5.1a CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/0:
FILING DATE: 12-SEP-1994
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   FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
  HYPOTHETICAL: N
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Local Similarity 55.6%;
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   REFERENCE/DOCKET NUMBER: 32,
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  STREET:
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  98101
   Seattle
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Gaps

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US-09-058-264-1
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GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,72
   TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
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TELEPHONE: (206) 587-0430
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OPERATING SYSTEM: Apple 7
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   APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/US95/06530
  APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Recepto
NUMBER OF SEQUENCES: 11
   NAME: Anderson, Kathryn A.
REGISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
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51 University Street
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  Conservative
   (206) 233-0644
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   CDS
244..2369
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   US 08/308,881
   Score 28.6; DB 3;
Pred. No. 1.2;
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  TELEFAX: (212)-997-10
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MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
  APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
   TELECOMMUNICATION INFORMATION: TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
   CORRESPONDENCE ADDRESS:
  ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford
REGISTRATION NUMBER: 32,
  CURRENT APPLICATION DATA:
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LENGTH: 3085 base pair
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   80 tattaactaaccatctttgccaatgttgcttaagctttt 118
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 222 TACTAATTTTGTGATTTGGAAATATCCGCGCAAGATGTT 260
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SOFTWARE: MS-DOS EDITOR
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  TOPOLOGY: un
   TYPE:
   REFERENCE/DOCKET NUMBER:
   CLASSIFICATION:
  ADDRESSEE:
   55; Conservative
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  New York
: New York
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   1140 Avenue of the Americas
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   244..309
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  Davidson, Davidson and Kappel, LLC
  JMBER: US/08/795,473B
11-FEB-1997
  Clifford M
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Pred. No. 1.2;
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  ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-6931
INFORMATION FOR SEQ ID NO: 79:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol L. Francis, Ph.D.
STREET: 285 Hamilton Ave, Suite 200
   GENERAL INFORMATION:
  APPLICANT: Stern, Robert
APPLICANT: Frost, Gregory
APPLICANT: Csoka, Anthony
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Human Plasma Hyaluronidase
NUMBER OF SEQUENCES: 10
   SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/781,891 FILING DATE: 27-DEC-1996 CLASSIFICATION: 800
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICANT:
APPLICANT:
APPLICANT:
  APPLICANT: Schelienberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
  Local 57;
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
   63 ttcctgactctgctatttattaactaaccatctttgcccaatgttg 107
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  STATE:
  CITY: Seattle
  STREET:
   ADDRESSEE:
   4Mar. 609062
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   98104-7092
   Washington
   Application US/08781891
  6300 Columbia Center, 701 Fifth Avenue
   Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
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   Mulligan, John T.
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   SEED and BERRY LLP
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LENGTH: 2517
  APPLICANT: Stern, Robert
APPLICANT: Csoka, Anthony
APPLICANT: Frost, Gregory I.
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Purification and Microsequencing of
TITLE OF INVENTION: Hylauronidase Isozymes
FILE REFERENCE: 9076/088CIP2
CURRENT APPLICATION NUMBER: US/08/987,743
CURRENT FILING DATE: 1997-12-09
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 17-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L.
REGISTRATION UMBER: 36,513
REFERENCE/DOCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
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LENGTH: 2517 base pairs
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  Sequence 4, Application US/08916935 Patent No. 6193963
  APPLICANT: Csoka, Anthony
APPLICANT: Wong, Tim. M.
TITLE OF INVENTION: Human Plasma Hyaluronidase
FILE REFERENCE: 9076-088CIP
CURRENT APPLICATION NUMBER: US/08/916,935
CURRENT FILING DATE: 1997-08-21
  GENERAL INFORMATION:
  APPLICANT: Stern, Robert
APPLICANT: Frost, Gregory I.
  SOFTWARE: FastSEQ for Windows Version 3.0
   NUMBER OF SEQ ID NOS: 11
   EARLIER APPLICATION NUMBER: 08/733,360 EARLIER FILING DATE: 1996-10-17
   APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: Mutations
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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FILING DATE: 19920810
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   ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
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  76 tatttattaactaaccatctttgccaatgttgcttaagct 115
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Miller, Suzanne E.
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TELEPHONE: 215-568-3100
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LENGTH: 5873 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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   GenCore version 4.5 (c) 1993 - 2000 Compugen
  100%
  Ltd.
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

| <b>98</b>          | ი ი<br>7 6 5                             | 4 3 2 1                                                                                            | Result      |
|--------------------|------------------------------------------|----------------------------------------------------------------------------------------------------|-------------|
| 35.2               | 35.8<br>8                                | 38.4<br>38.4<br>35.8                                                                               | Score       |
| 7052 21<br>9519 22 | 13046 22<br>160755 23<br>162450 21       | 32.0 9614 22 ABA15/90<br>32.0 9614 22 ABA15792<br>30.0 59060 22 AAK85994<br>29.8 13046 22 AAL03250 | Length DB I |
| Human musculoskele | Human DNA for a no<br>Human DNA sequence | Human nervous syst Human nervous syst Human immune/haema. Human reproductive                       | Description |

31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000;

; 2000US-0179065. ; 2000US-0180628. ; 2000US-0184664. ; 2000US-0186350. ; 2000US-0189874. ; 2000US-0190076.

| (          | ٠        | C        | C                 | C                  | C        | a                  | a                  | o                  |                    |                    |                    | C        |                   |                    |                    | O                  | a                  | O                 |                    |                    |                   | O                  |                    |                    |                    |                    |                    | O                  | O                  |                    |                    |                    |                    |                    | O                 |
|------------|----------|----------|-------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| 4.5        | ^        | 43       | 42                | 41                 | 40       | 39                 | 38                 | 37                 | 36                 | <u>3</u> 5         | 34                 | 33       | 32                | 31                 | 30                 | 29                 | 28                 | 27                | 26                 | 25                 | 24                | 23                 | 22                 | 21                 | 20                 | 19                 | 18                 | 17                 | 16                 | 15                 | 14                 | 13                 | 12                 | 11                 | 10                |
| 32.2       | J        |          | Ν.                | 2                  |          |                    |                    |                    | 2                  | 2                  | 2                  | 32.6     | 2                 | 2                  | 2                  | w                  | w                  | 33.4              | $\omega$           | ω                  | ω                 | w<br>•             | w                  | ω                  | ω                  | 34                 | 34                 | 4                  | 34.2               | 4                  | 4                  | 4                  | Ú                  | Ġ                  | Ú.                |
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| 2035       | 1497     | 792      | 575               | 575                | 575      | 575                | 575                | 575                | 200                | 10085              | 10085              | 2496     | 1964              | 1427               | 613                | 39796              | 11130              | 23071             | 19301              | 19301              | 17425             | 5845               | 5424               | 5424               | 3952               | 22473              | 615                | 15944              | 13819              | 4171               | 305                | 267                | 4.1                | 56632              | _                 |
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| YSK1 prote | TANG     |          | Probe #10103 used | Probe #7040 for ge |          | Human brain expres | Probe #7696 for ge | Human foetal liver | CFTR gene regulato | Human reproductive | Genomic sequence # |          | Human full-length | Human secreted pro | Human immune/haema | Nucleotide sequenc | Human nervous syst | Human genomic DNA | Human adenosine re | Human low adenosin | Human Stat6 gene. | Human immune syste | Human adenosine re | Human low adenosin | Human lung antigen | Human immune/haema | Human immune/haema | Human nervous syst | Human nervous syst | Human musculoskele | Human breast cance | Human breast cance | Human ABC1 genomic | Human immune/haema | Tumour suppressor |

## ALIGNMENTS

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Human nervous system related polynucleotide SEQ ID NO 8121.
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  ABA15790 standard; DNA; 9613
  (first entry)
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08-NOV-2000

017-NOV-2000

17-NOV-2000

17-N
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
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   Ö
   SCI INC
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   1701pp +
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   Sequence Listing; English.
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ABA15792
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ABA167
AC ABA1
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   isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthitis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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18-APR-2000;
19-MAY-2000;
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8888888**x**&

(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

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08-DEC-2000
                                 The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, allergies, autoimmune themselves and the second of the cancer of the advisors, autoimmune themselves and the second of the cancer of the advisors, autoimmune themselves and the second of the cancer of the advisors, allergies, autoimmune themselves and the second of the cancer of the advisors, allergies, autoimmune themselves and the second of the cancer of the second of the cancer of the advisors, allergies, autoimmune themselves and the second of the cancer of the second of the cancer of the advisors, allergies, autoimmune themselves and the second of the cancer of the second of the cancer of the advisors, allergies, autoimmune themselves and the second of the cancer of the second of the cancer of the advisors, and the second of the cancer of the advisors of 
   Disclosure; SEQ ID NO 8123; 1701pp + Sequence Listing; English.
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  cancers and
  Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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  SM;
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Conservative

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Mismatches

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Score 38.4; DB Pred. No. 0.016;

Length 9614; Indels

Match 32.0%; Local Similarity 62.5%;

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ВP

cytostatic; gene therapy; vaccine; metastasis;

Human immune/haematopoietic 07-NOV-2001 (first entry)

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

antigen genomic sequence SEQ ID NO:40806

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   17-JAN-2001;
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colitis;

multiple sclerosis, rheumato (c) cardiovascular disorders

rheumatoid arthritis and ulcerative

such

as myocardial

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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) cartivity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnosis and camber of diseases associated with inappropriate (I) expression. For cerample, they may be used to treat discorders associated with decreased cexample, they may be used to treat discorders associated with decreased conversion by rectifying mutations or deletions in a patient's genome cc that affect the activity of (I) by expressing inactive proteins or to converse the patients own production of (I). Additionally, (I) converse and treat immune/haematopoietic-related (I), by inserting converse and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 converse from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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17-NOV-2000;
   Disclosure; SEQ ID NO 40806; 3071pp + Sequence Listing; English.
  Nucleic acids encoding useful for preventing, metastasis -
  WPI;
   Rosen
   ( HUMA-)
   17-NOV-2000;
17-NOV-2000;
  2001-483426/52.
  CA,
   HUMAN GENOME
  Barash
   2000US-0246611.
2000US-0246613.
2000US-0249207.
   2000US-0249217

2000US-0249218

2000US-0249245

2000US-0249245

2000US-0249265

2000US-0249265

2000US-0249297

2000US-0249297

2000US-0249309

2000US-0250160

2000US-0251030

2000US-02511030

2000US-02511030

2000US-02511868

2000US-02511868

2000US-02511868

2000US-02511868

2000US-02511869

  2000US-0249213.
2000US-0249214.
2000US-0249215.
2000US-0249216.
  2000US-0249210.
2000US-0249211.
2000US-0249212.
   2000US-0249209
  SC,
   SCI INC
   human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
   Ruben
   SM
```

Query Match Best Local Matches

Similarity

58 58

. 3%;

Score 36; DB Pred. No. 0.17 0; Mismatches

Conservative

0,

45;

0;

Gaps

0

Length 59060; Indels

13 gtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactc

Sequence

59060

ВP;

14758 A;

13705

Ç; 13620

G; 16977

T; 0 other;

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RESULT AALO ID ALO ID A
   밁
  Ş
   멍
         31-JAN-2000

04-FEB-2000

24-FEB-2000

16-MAR-2000

17-MAR-2000

17-MAR-2000

19-MAY-2000

07-JUL-2000

07-JUL-2000

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11-JUL-2000

11-JUL-2000

14-JUL-2000

14-JUL-2000

14-AUG-2000

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   10148 tgctgttcatttcccacgtggccttgaacaagctgcttcccctctctt 10195
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  17-JAN-2001;
  02-AUG-2001.
   WO200155320-A2.
   Homo sapiens.
   Human; reproductive system related antigen; reproductive system disorder;
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   21-NOV-2001 (first entry)
  AAL03250;
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   73 tgctatttattaactaaccatctttgccaatgttgcttaagctttttt 120
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2000US-0214886

2000US-0214880

2000US-0214880

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2000US-0217487

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  2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
  2000US-0225266.
2000US-0225267.
  2001WO-US01339.
  NO: 5938.
      14 - SEP-2000;
14 - SEP-2000;
14 - SEP-2000;
21 - SEP-2000;
21 - SEP-2000;
25 - SEP-2000;
25 - SEP-2000;
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29 - SEP-2000;
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21 - N
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11-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
2000US-0235834.
2000US-0235836.
2000US-0236367.
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2000US-0237039.
2000US-0241785.
2000US-0241785.
2000US-0241808.
2000US-0244617.
2000US-0246475.
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2000US-0246477.
2000US-0246477.
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   2000US-0231243.
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2000US-0231244.
2000US-0231414.
2000US-0231414.
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2000US-0232397.
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2000US-0232398.
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2000US-02323401.
2000US-02323401.
2000US-02334063.
  2000US-0233064
2000US-0233065
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Matches
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08-DEC-2000
08-DEC-2000
08-DEC-2000
  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
  WPI;
  5000 actgtgtgaccttgggcaagttacttagcttctct 5034
   4940 aaaagcacggactctggaaccagtctgtctgaatttgaatcctagctctgccaattacta 4999
   Sequence 13046 BP;
  Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a | medical condition
   Rosen
   (HUMA-) HUMAN GENOME SCI INC
  05-JAN-2001;
               human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections;
   Human; secreted extracellular matrix protein; ds; immunomodulatory; Anti-HU; antianemic; antischeumatic; antischerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
  04-DEC-2001
   AAS31516;
   AAS31516 standard; DNA; 13046 BP
  17-NOV-2000;
  Human DNA
   85 actaaccatctttgccaatgttgcttaagcttttt 119
   Local
  2001-465570/50.
  58;
   Similarity
  for a novel extracellular matrix protein,
   Barash SC,
  SEQ ID NO 5938; 1297pp + Sequence Listing;
  2000US-025198
2000US-025198
2000US-0256719
2000US-0251479
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2000US-0251990
2000US-0251997
2000US-0251997
2000US-0251997
  2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249300.
  Conservative
   (first entry)
  2000US-0250160
2000US-0250391
 immunogen;
   3599 A; 2614 C;
  29.8%;
61.1%;
  Ruben
   gene
  Score 35.8; DB Pred. No. 0.12; 0; Mismatches
  0;
  SM;
therapy;
   2885
   G; 3948
    antisense;
  DB 22;
  37; | Indels
   Ŧ
  Length 13046;
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  Seq ID No
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  English.
      additive
  0;
   595.
  Gaps
  0;
      14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

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22-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

23-AUG-2000

21-SEP-2000

01-SEP-2000

   14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
   30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
   14-SEP-2000;
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14-SEP-2000;
   Homo sapiens.
   14-AUG-2000;
14-AUG-2000;
  07-JUN-2000;
   17-JAN-2001;
  02-AUG-2001
  WO200155368-A1
  11-JUL-2000;
   19-MAY-2000;
  18-APR-2000;
  17-MAR-2000;
  16-MAR-2000;
   2000US-0190076.
2000US-0198123.
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2000US-0209467.
2000US-0211647.
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2000US-0211496.
2000US-0211496.
2000US-0211496.
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2000US-02154519.
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2000US-0225213.
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2000US-0230437.
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2000US-0231242.
2000US-0231244.
  2000US-0225267.
2000US-0225268.
2000US-0225270.
   2001WO-US01348
   2000US-0229287
2000US-0229343
   2000US-0227009
2000US-0228924
   2000US-0226868.
2000US-0227182.
  2000US-0226681
  2000US-0225759
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  2000US-0225758
   2000US-0225757
  2000US-0225266
  2000US-0186350
2000US-0189874
  2000US-0184664
   2000US-0179065
  2000US-0233063.
2000US-0233064.
  2000US-0232081
  2000US-0229345
   2000US-0231968
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Ş 밁

29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000;

2000US-0240960 2000US-0239937 2000US-0239935 2000US-0237040 2000US-0237039

2000US-0236802. 2000US-0237037. 2000US-0237038.

```
RESULT 6
AAH88704/c
Qy
   Дb
  Ωy
   Delynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of Sps. The Sp polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of Sps by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The Sps may also be used as natigens to produce antibodies and to identify modulators (agonists and antagonists) of the Sps. The anti-(Sp) antibodies and antagonists and antagonists for detecting the presence of Sps in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. morphasms of the breast or liver, Sezary syndrome and Sarkinson's disease) neurological diseases (e.g. Allzheimer's disease, arrest technorardia and analysing infections and whither is disease.
   Matches
   Query Match
Best Local
             13-JAN-2000; 2000US-0175854
   8107 AAAAGCACGGACTCTGGAACCAGTCTGTCTGAATTTGAATCCTAGCTCTGCCAATTACTA 8048
   11-JAN-2001; 2001WO-IB00116
  8047 ACTGTGTGACCTTGGGCAAGTTACTTAGCTTCTCT 8013
  19-JUL-2001
   WO200151659-A2
  central nervous system disorder; CNS;
  Single nucleotide polymorphism; SNP; biallelic marker;
   Human DNA sequence SEQ ID 544.
   26-FEB-2002 (first entry)
  AAH88704;
   AAH88704 standard; DNA; 160755 BP
   Homo sapiens
  Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
  include
  The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The
   Claim 1; SEQ ID No 595; 577pp; English.
  (HUMA-) HUMAN GENOME SCI INC
  85 actaaccatctttgccaatgttgcttaagcttttt 119
  est, tachycardia and angina), infections caused by bacteria, viruses fungi and ocular disorders (e.g. corneal infections). Other uses lude wound healing, maintenance of organs before transplantation, port of cell culture of primary tissues, modulation of for example
   Similarity 61.: 58; Conservative
  Barash SC,
   29.8%;
61.1%;
  Ruben SM
   0,
   Score 35.8; DB 22; Pred. No. 0.12;
   Mismatches
   No.
   37;
   Length 13046;
  human;
  0;
  Gaps
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0,

2000US-0246611. 2000US-0246609. 2000US-0246610. 2000US-0246532 2000US-0246609

13-OCT 2000
13-OCT 2000
20-OCT 
2000US-0246526. 2000US-0246527. 2000US-0246528.

2000US-0241221 2000US-0241785 2000US-0241786 2000US-0241786 2000US-0241808 2000US-0241809 2000US-0241826 2000US-0241826 2000US-0246477 2000US-0246474 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477

17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 01-DEC-2000 01-DEC-2000 05-DEC-2000 05-DEC-2000 05-DEC-2000 06-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000

2000US-0250391
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2000US-0251988
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2000US-0251869
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2000US-0251989
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2000US-0251989

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249216. 2000US-0249217. 2000US-0249214. 2000US-0249215. 2000US-0249212

17-NOV-2000; 17-NOV-2000;

2000US-0249218. 2000US-0249244. 2000US-0249264. 2000US-0249264. 2000US-0249264. 2000US-0249297. 2000US-0249299. 2000US-0249299.

GENSET

```
Š
  Db 144713
  Db 144773
   Matches
   Query Match
Best Local
  The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders (see AAH88161-AAH88702). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used to illustrate the invention.
  Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker \dot{\ }_{\ |}
  Disclosure;
  RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
  AAZ86967;
  Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727
  WPI; 2001-483085/52.
   (GEST )
              diseases, especially those differentiation -
  30-JUN-1998;
10-DEC-1998;
  06-JAN-2000
  Retinoblastoma binding protein-7 genomic DNA sequence.
  AAZ86967 standard; DNA; 162450
                                      Novel nucleic acid and polymorphic markers used
   Bougueleret L;
   30-JUN-1999;
  WO200000607-A1
  Homo sapiens.
  16-MAY-2000
  (GEST ) GENSET
  lymphoma; ds.
  69
   9 gggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctg 68
  7
  GCTCTGCTACTTACTGGCTGGGAGTTTCACCTGTTTGGGCCCTCAGTTTTCT 144663
  actctgctatttattaactaaccatctttgccaatgttgcttaagcttttt 119
  GTGGATGTTGCTAAGATAGAGCATGGACTTTGAAACCAGATTAACTGCATCTGAAGCCTG
   2000-117170/10
   64;
   Similarity
  Blumenfeld M,
  Page 476-519; 519pp; English.
   Conservative
  (first entry)
  98US-0091315.
98US-0111909.
   99WO-IB01242
  29.8%;
57.7%;
  Cohen
                           involving
   0;
  Score 35.8;
Pred. No. 0.
  ū
  ВP
  Mismatches
                             abnormal cell
   .27;
  DB
   47;
   23;
                           for diagnosis of
ell proliferation
  Indels
   |Length 160755;
   T; 181 other;
   0; Gaps
                              and
  144714
  0,
```

```
RESULT
AAC69140
  Вþ
  QУ
  Вþ
  Qγ
   Matches
   Query Match
Best Local
   82463 ctgtgtgatcttgggatggttacttaatctttt 82495
   82403 atagtatgaactgtggagccagttggtctgggtttgaatcctggctctgccacttccttg 82462
   This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g. AAZ87035-Z87099) are useful for DNA amplification and detection methods. RBP-7 biallelic markers (see AAZ8693-Z87034) are useful for diagnosis of disease related to alteration in the regulation or in the coding regions of the RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include the process of the contract of the cont
   15-MAR-1999;
08-JUN-1999;
17-JUN-1999;
   thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers, including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukaemias, and
   cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ds.
   Human ABC1 cholesterol transporter; chromosome 9931;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangler disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
  Claim
  Human ABC1 gene exons 23-28.
  AAC69140;
   AAC69140 standard; DNA; 7052 BP
  Sequence 162450 BP; 45465 A; 30661 C; 32637 G;
   lymphomas. RBP-7
                           WPI; 2000-587528/55
   Hayden MR,
  (UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON BIORESEARCH INC.
   21-SEP-2000
   WO200055318-A2
   Homo
  29-JAN-2001
   15-MAR-2000;
  œ
   sapiens.
  ctaaccatctttgccaatgttgcttaagctttt 118
  1; Page 118-163; 223pp; English
   l Similarity
57; Conser
   Conservative
  Wilson AR,
  (first entry)
   2000WO-IB00532
  99US-0124702.
99US-0138048.
99US-0139600.
99US-0151977.
  antibodies are useful as diagnostic agents.
   29.5%;
  Pimstone
   0;
  Score 35.4; DB Pred. No. 0.36;
   Mismatches
  DB
   21;
   36;
  53673 T; 14 other;
   Indels
  Length 162450;
   0;
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0;

```
RESULT
AAL37169
      밁
  δÃ
   В
   Š
   CC disease, particularly coronary artery disease, but also cerebrovascular CC disease, coronary restenosis, and peripheral vascular disease.

CC conversely, a high level of HDL has protective effects against CC conversely, a high level of HDL has protective effects against CC cardiovascular disease. The invention provides genetic constructs and CC transgenic cells and non-human animals comprising human ABC1 nucleic CC acids, and methods of gene therapy for the treatment or prevention of CC cerediovascular disease compounds the administration of an expression CC encompasses compounds which mimic ABC1 activity, compounds which CC stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the CC carebrovascular disease, especially coronary artery disease, CC cerebrovascular disease, especially coronary artery disease, CC cerebrovascular disease, especially coronary artery disease, CC cerebrovascular disease, coronary restenosis or peripheral vascular CC disease. They may also be used in the treatment of disease associated CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid cacid with the exact sequence as GenBank Accession No: CAB10005.1 and X75926, and the nucleic CC The present sequence represents a fragment of the human ABC1 gene
  Matches
   Query Match
              Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antipungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder
  Human musculoskeletal system related polynucleotide SEQ ID NO 3534.
  08-JAN-2002 (first entry)
  AAL37169;
   AAL37169 standard;
   5906 gaccttgggcaagctgcttagtctctct 5933
  5846 gggagtttggagcatacagagctcaagttgaatcctgactttgctacttattggctatat 5905
      neurological disease;
   Sequence 7052 BP; 1816 A; 1465 C; 1725
   comprising exonic sequences.
   involved in cholesterol efflux from the cell. The gene encoding ABCl is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular
  The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the AFP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being
   Disclosure; Fig 12; 229pp; English.
   disease
   New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
   92 atctttgccaatgttgcttaagcttttt 119
  Local
   9
  55;
  Similarity
   and
  Conservative
   cancer
   DNA;
   29.3%;
    infection; human;
   9519 BP
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   Score 35.2; DB Pred. No. 0.16;
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  11-JUL-2000
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   18-APR-2000
   16-MAR-2000;
17-MAR-2000;
  17-JAN-2001; 2001WO-US01338
  02-AUG-2001.
  musculoskeletal system; ds.
   Homo sapiens.
  2000US-0232400.
2000US-0232401.
2000US-0233063.
   2000US-0225213
2000US-0225214
2000US-0225266
2000US-0225267
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2000US-0225270
2000US-0225247
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2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0231242.
2000US-0231243.
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  2000US-0233064
  2000US-0231968
  2000US-0229513.
2000US-0230437.
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2000US-0229344.
  2000US-0227009.
2000US-0228924.
2000US-0229287.
  2000US-0226279.
2000US-0226681.
   2000us-0232399
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2000US-0232398
  2000US-0232081
  2000US-0231244
   2000US-0229345
2000US-0229509
   2000US-0226868
2000US-0227182
   2000US-0225758.
2000US-0225759.
   2000US-0224518
2000US-0224519
   2000US-0220964
  2000US-0205515.
2000US-0209467.
   2000US-0190076.
2000US-0198123.
  2000US-0220963
   2000US-0215135
   2000US
   2000US-0189874
  2000US-0184664
  -0214886
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20-OCT-2000;
20-OCT-2000;
  29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
  25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
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02-OCT-2000;
   08-NOV-2000;
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  20-OCT-2000;
   13-OCT-2000;
  13-OCT-2000;
   02-OCT-2000;
  29-SEP-2000;
  17-NOV-2000;
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  17-NOV-2000;
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  17-NOV-2000;
  17-NOV-2000;
   17-NOV-2000;
  17-NOV-2000;
   2000US-0234998.
2000US-0235484.
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2000US-0235836.
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2000US-0236370.
2000US-0236370.
2000US-0236370.
2000US-0236370.
                                   2000US-0249245

2000US-0249264

2000US-0249265

2000US-0249297

2000US-0249390

2000US-0249390

2000US-0250160

2000US-0250160

2000US-02501391

2000US-0251988

2000US-0251988

2000US-0251868

2000US-0251868

2000US-0251868
  2000US-0240960.
2000US-0241221.
   2000US-0237040.
2000US-0239935.
   2000US-0237038
2000US-0237039
  2000US-0246475
  2000US-0241787.
2000US-0241808.
  2000US-0239937
  2000US-0246478.
   2000US-0246474.
   2000US-0244617
   2000US-0241826
   2000US-0241809.
   2000US-0241785.
   2000US-0249214
   2000US-0249213
  2000US-0249211
   2000US-0249210
   2000US-0249209
  2000US-0246613
   2000US-0246611
   2000US-0246610
   2000US-0246609
   2000US-0246532
  2000US-0246526
  2000US-0246525.
   2000US-0246524.
   2000US-0246523
   2000US-0246477.
```

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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (antjagonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC corrections diseases such as myocardial ischaemias; (d) wound CC cardiovascular diseases such as viral, bacterial, fungal and corrections diseases such as viral, bacterial, fungal and
   Query Match
Best Local
   Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} 
  diagnosis -
  Sequence 9519 BP; 2702 A; 1682 C; 1664 G; 3471 T; 0 other;
  parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
   Example 2; SEQ ID
   (HUMA-) HUMAN GENOME SCI INC
  from WIPO at ftp.wipo.int/pub/published_pct_sequences.
  Match 29.3%;
Local Similarity 62.5%;
   2001-451937/48.
   Barash SC,
   NO 3534;
   Ruben SM;
   781pp + Sequence Listing; English
Score 35.2; DB Pred. No. 0.18; 0; Mismatches
   DB 22;
  Length 9519;
```

```
RESULT 10
AAS46356/c
  Matches
                 Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
  Tumour suppressor gene derived chemically modified sequence #78
   AAS46356 standard; DNA; 14537 BP
   3888
cytosine methylation; ds.
  AAS46356;
   3948 tctgccacttagtagccatgtgaatttg 3975
   18-DEC-2001 (first entry)
  11 gggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgac
  71 tctgctatttattaactaaccatctttg 98
  gggtattgctggcctagagtatagactctggagctagactgcctatgtttgaatcctggc 3947
  Conservative
  0;
  33;
  Indels
  0;
  Gaps
  70
  0;
```

Ω Dр QΥ

Homo sapiens.

WO200168912-A2

15-MAR-2000; 2000DE-1013847 15-MAR-2001; 2001WO-EP02955 20-SEP-2001

```
RESULT
AAK65581
  Ş
   Дb
  The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC (SS) and sequences complementary to (SS). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC carray for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for assertaining genetic and/or epigenetic parameters for the diagnosis CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC differences serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC complementary sequences derived from tumour suppressor genes and CC complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence (s.g. is missing).
  Query Match
Best Local Similarity
   Matches
      cytostatic; gene therapy; vaccine;
             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20393.
  1276
   06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
  06-NOV-2001
  AAK65581;
  AAK65581 standard;
  1336
  Sequence 14537 BP; 3628 A; 495 C; 3778 G; 6636 T; 0 other
   of the printed specification, but was obtained in format directly from WIPO at
  Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
  ftp.wipo.int/pub/published_pct_sequences.
  Note: The sequence data for this patent did not form part
   is missing)
  Claim 1; SEQ ID No 78; 27pp; English.
  WPI; 2001-602752/68.
   Olek A,
  (EPIG-) EPIGENOMICS AG.
   11
  80 tattaactaaccatctttgccaatgttgcttaagct 115
  20
  atagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatt 79
   TATTAACAATATAACCTTAAATAAATTACTTAATCT 1241
  58;
  Piepenbrock C,
  Conservative
   (first entry)
   2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
   DNA; 56632 BP
   29.3%;
   Berlin
   Score 35.2; DB Pred. No. 0.2; 0; Mismatches
  0;
     metastasis;
  38;
   22;
  Length 14537;
  electronic
  Indels
   0;
   Gaps
  0;
 PP PN XX
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
  05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

11-SEP-2000

11-SEP-2000

11-SEP-2000
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01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
   22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
  14-SEP-2000;
14-SEP-2000;
  30-JUN-2000;
07-JUL-2000;
   14-AUG-2000;
   14 - AUG - 2000;
   07-JUL-
   24-FEB-2000;
02-MAR-2000;
  17-JAN-2001;
  WO200157182-A2
   19-MAY-
  17-MAR-2000
  16-MAR-2000;
   09-AUG-2001.
  Homo sapiens.
             2000US-0234223.
2000US-0234274.
2000US-0234997.
  2000US-0233063.
2000US-0233064.
2000US-0233065.
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2000US-0229344
2000US-0229345
2000US-0229509
2000US-0229513
2000US-0230437
2000US-0230438
2000US-0231242
2000US-0231243
  2000US-0226868.
2000US-0227182.
2000US-0227009.
  2000US-0179065.

2000US-0180628.

2000US-0184664.

2000US-0186350.

2000US-0189874.

2000US-0199076.

2000US-0199123.

2000US-0205515.

2000US-0209467.
  2000US-022
  2000US-02
2000US-02
   2000US-0231968.
2000US-0232397.
  2000US-0228924.
2000US-0229287.
   2000US-0232401
  2000US-0232400
   2000US-0232398
  2000US-0232080.
2000US-0232081.
   2000US-0231413.
2000US-0231414.
  2000US-0231244.
   2000US-0225214
2000US-0225266
  2000US-0224519
2000US-0225213
  2000US-0217496.
2000US-0218290.
  2000US-0224518
   2000US-0
  2000US
  2001WO-US01354
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13-OCT-2000;
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20-OCT-2000;
  26-SEP-2000;
27-SEP-2000;
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  20-OCT-2000;
20-OCT-2000;
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  17-NOV-2000;
  17-NOV-200
  2000US-0240960.
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2000US-0241785.
  2000US-0249264.
2000US-0249265.
2000US-0249297.
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  2000US-0249212.
2000US-0249213.
2000US-0249214.
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2000US-0249215.
   2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0246610.
   2000US-0235484.
2000US-0235834.
   2000US-0241808.
2000US-0241809.
   2000US-0239937.
   2000US-0237040
  2000US-0236369
   2000US-0236368.
   2000US-0249245
  2000US-0249244.
  2000US-0249217
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  2000US-0249209
2000US-0249210
   2000US-0249207
2000US-0249208
   2000US-0246611.
  2000US-0246528
   2000US-0246527
   2000US-0246526
  2000US-0246478.
2000US-0246523.
  2000US-0246476
   2000US-0246475
   2000US-0246474.
   2000US-0244617
  2000US-0241826
  2000US-0246525
   -0246613
```

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RESULT :
   밁
   δõ
   В
  οy
   CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) creatment of diseases associated with inappropriate (I) expression. For ce example, they may be used to treat disorders associated with decreased ce expression by rectifying mutations or deletions in a patient's genome cc supplement the activity of (I) by expressing inactive proteins or to conclude may be used to produce the secreted (I), by inserting cc polynucleotides may be used to produce the secreted (I), by inserting cc protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting cc diagnose and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic cc sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
Query Match
Best Local
  Matches
   51064 tctgccacttagtagccatgtgaatttg 51091
  01-SEP-1999;
15-MAR-2000;
23-JUN-2000;
   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
   Disclosure;
  metastasis
  WPI; 2001-483426/52.
  High density lipoprotein-cholesterol; HDL-C;
  Sequence 56632 BP; 17016 A; 8910 C; 10552 G; 20154 T; 0 other;
  (HUMA-) HUMAN GENOME SCI INC.
  Human ABC1 genomic DNA.
   AAF92831 standard; DNA; 183999 BP
   01-SEP-2000; 2000WO-IB01492
   08-MAR-2001
  WO200115676-A2
  Homo sapiens.
  17-MAY-2001 (first entry)
          (UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON GENETICS INC.
  71 tctgctatttattaactaaccatctttg 98
  55;
   Similarity
   Barash SC,
   SEQ ID NO 20393; 3071pp + Sequence Listing; English.
  ; 99US-0151977.
; 2000US-0526193.
; 2000US-0213958.
  Conservative
   29.3%;
  Ruben SM;
   0,
   Score 35.2; D
Pred. No. 0.3;
   Mismatches
  DB
   33
•
  cardiovascular; ABC1;
  Length 56632;
   0,
   Gaps
   ds
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0;

```
δÃ
  Db 145152 gggagtttggagcatacagagctcaagttgaatcctgactttgctacttattggctatat 145211
   Qy
  В
   145212 gaccttgggcaagctgcttagtctctct 145239
   14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
    New peptide useful as a
                               WPI; 2001-451856/48.
   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
  15-MAY-2000;
  14-JAN-2000;
   10-JAN-2001; 2001WO-US00798
   19-JUL-2001.
   Human breast cancer expressed polynucleotide 5722.
  The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition sele lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
   Human; breast cancer; cell marker; cytostatic; ss
  07-DEC-2001
  AAL13265 standard; cDNA;
   Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other:
  Claim 8; Fig 1; 317pp; English.
   Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates or RXR-mediated transcriptional activity -
  Treating
   WPI; 2001-244356/25.
   92
   atctttgccaatgttgcttaagcttttt 119
   Similarity
  Xu Y,
   2000US-0189167
2000US-0192099
2000US-0193480
2000US-0205230
2000US-02213315
2000US-0220534
   Conservative
   2000US-0176077
  Brooks-Wilson
   (first entry)
  Wang
  29.3%;
  Y,
    marker
  AR,
   0;
   ВP
  Score 35.2; DB Pred. No. 0.43; D; Mismatches
for the diagnosis
  Pimstone SN,
  compound that modulates
  33;
   22;
   Clee
of breast cancer
  Indels
  Length 183999;
   0,:
  ۵
   0;
```

```
RESULT 14
AAL22135
  밁
   δÃ
   Вb
   QΥ
   Matches
  Query Match
       The invention relates to human breast cancer expressed polynucleotides (AALD7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for
   14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
  New peptide useful as a marker for the diagnosis of breast cancer
   WPI; 2001-451856/48.
  Lillie J,
   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
  The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
  15-MAY-2000;
  10-JAN-2001; 2001WO-US00798
   WO200151628-A2
   Human; breast cancer; cell marker; cytostatic; ss
  Human breast cancer expressed polynucleotide 14592.
  07-DEC-2001
   AAL22135 standard; cDNA;
   AAL22135;
  Sequence 267 BP; 77 A;
   Claim 1; Page 1029; 3695pp; English.
  91 acttacttactaatattct 109
   31
   17
  77 atttattaactaaccatct
  Local
   ggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgct 76
   999aaaaaaatcgtggaattttggagacaaacaaatccacgtntaaatcctcactttgct 90
  Similarity
   Xu Y, Wang Y,
   ; 2000US-0189167.
2000US-0192099.
2000US-0193480.
2000US-0205230.
2000US-0205230.
2000US-0211315.
2000US-0220534.
  Conservative
  2000US-0176077
   (first entry)
  2627; 3695pp; English
  29.0%;
monitoring, characterising treating
  46 C;
  305
   95
  Steinmann
  0;
   Score 34.8; D
Pred. No. 0.08
0; Mismatches
  ВÞ
  51 G;
  90 T; 3 other;
   .08;
  DB
   28;
   Length
  Indels
  267;
   0;
  Gaps
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0;

```
RESULT 1
AAL36300
  밁
   Š
   밁
   δÃ
  SSSSS
    Query Match
Best Local
   Matches
18 APR-2000

19 MAY - 2000)

07 - JUN - 2000)

28 - JUN - 2000)

07 - JUL - 2000)

07 - JUL - 2000)

11 - JUL - 2000)

11 - JUL - 2000)

14 - JUL - 2000)

14 - JUL - 2000)

14 - AUG - 2000)
   31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
  potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antialabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
  Human musculoskeletal system related polynucleotide SEQ ID
  08-JAN-2002 (first entry)
   AAL36300;
  AAL36300 standard; DNA; 4171 BP
  Sequence 305
  16-MAR-2000;
17-MAR-2000;
  17-JAN-2001;
   02-AUG-2001.
  WO200155367-A1
   Homo
  17
  91
  77
   31
   15
   ggcatagaaagagcaggaccttgggagcaagaatatctaagttttaattcctgactctgct
   sapiens.
   gggaaaaaaatcgtggaattttggagacaaacaaatccacgtctaaatcctcactttgct
  Similarity
 2000US-0179065
2000US-0184664
2000US-0184664
2000US-0184664
2000US-0198174
2000US-0199174
2000US-0199123
2000US-0199123
2000US-0214886
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2000US-0211647
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2000US-02116480
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2000US-02285270
2000US-02285270
2000US-02285270
2000US-02285277
   Conservative
  BP;
  2001WO-US01338
  87
  Ą
  28.5%;
  54 C;
   0;
   Score 34.2; DB 22;
Pred. No. 0.13;
0; Mismatches 28;
  65
  G;
  99
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Barash SC, Ruben SM;

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

Example 2; SEQ ID NO 2665; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins C (ABB30387-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by C protein or gene therapy. The genes are isolated from a range of human it issues disclosed in the specification. The nucleic acids, proteins, and prevention of: (a) cancer, e.g. breast and ovarian cancer and contribodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and cother cancers of the adrenal gland, bone, bone marrow, breast, and other cancers of the adrenal gland, bone, bone marrow, breast, and discontestinal tract, liver, lung, or urogenital; (b) immune assimilation of discase, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, cultiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discorders such as myocardial ischaemias; (d) wound the line; (e) neurological diseases e.g. cerebral anoxia and epilepsy; caractivity infectious diseases such as viral, bacterial, fungal and

parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published\_pct\_sequences. format directly

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Дb Š

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Listing first 45 s
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  JOURNAL
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Rudert,F.H.
Direct Submission
Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
  H.sapiens CD95 gene
X87625
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2344)
Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
   Identification of a silencer, enhancer, in the human CD95 (Fas/APO-1) gene DNA Cell Biol. 14 (11), 931-937 (1995)
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: MBL; SW:,
  1 taggggaaggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagttt 60
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   Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
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  Blakey,S
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 1 03-FEB-2000;
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   http://www.sanger.ac.uk/HGP/Chr10
RP11-399019 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see,
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
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AB053451
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Location/Qualifiers
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   Yang,Y.G., Ohta,S., Yamada,S., Shimizu,M
Diversity of T cell receptor delta-chain
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Thome,A., Saalmuller,A. and Pfaff,E.
Molecular cloning of porcine T cell receptor alpha, beta,
Molecular cloning of porcine T cell receptor alpha, beta,
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  submitted (10-JAN-2001) Hirohide Uenishi, National Institute of Animal Industry, MAFF, Department of Animal Breeding and Genetics; P.O. Box 5, Tsukuba 305-0901, Japan (E-mail:huenishi@affrc.go.jp, Tel:81-298-38-8627, Fax:81-298-38-8793)
  porcine TCR gene alpha/delta locus
Unpublished
   Direct Submission
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  Direct Submission
Submitted (29-NOV-2000) Genome
University School of Medicine,
  Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
  Waterston, R.
   MO 63108,
   Waterston, R.H.
  Waterston, R.H.
  The sequence of Homo sapiens clone
   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   Unpublished
  Waterston, R.H
  Homo sapiens
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Homo sapiens chromosome 7 clone RP11-801B4, complete sequence.
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   Gaps
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0,

Louis

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Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:12964290.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
  GCTACCTAACTTTGGGCAAGTTTCTTTAACCTCT 10735
   65;
   University, 4444 Forest Park Avenue, St. 5 (bases 1 to 166847)
   Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Nov 29, 2000 this sequence version replaced gi:11128450.
   AL355852 128765 bp DNA | linear PRI Human DNA sequence from clone RP11-403E24 on chromosome
   Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
  Center: Washington University Genome Sequencing Center Center code: WUGSC
  Waterston, R.H.
   HTG
   sequence.
  Center project name: H_NH0801B04
   Direct Submission
   AL355852.23
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  Direct Submission
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69.1%;
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  32820 g 53946 t
   Genome Center -----
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  DB 9;
  29;
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  in the feature table with their source databases: Em:, EMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
   RP11-403E24 It may be shorter because we sequence overlapping RP11-403E24 It may be shorter because we sequence overlap; sections only once, except for a 100 base overlap. The true left end of clone RP11-403E24 is at 1 in this sequence. The true left end of clone RP11-284B18 is at 128666 in this sequence. The true right end of clone RP11-33N11 is at 69175 in
   Group.
  this sequence
  	ext{RP11-403E24} is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
  http://www.sanger.ac.uk/HGP/ChrX
  chromosome X,
  http://www.chori.org/bacpac/home.htm
  IMPORTANT: This sequence is not the entire insert of clone
  Further information can be found at
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                 Direct Submission
Submitted (20-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
CHEMISTRY: Dye-terminator Big Dye; 29% of reads Assembly program: Phrap; version 0.990319
   Web site:http://genome.wustl.edu/gsc/index.shtml
  Center: Washington University Genome Sequencing Center Code: WUGSC
   MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:6606060
  Waterston, R.H.
  162043 bp DNA linear HTG 07-. HOMO sapiens chromosome 11 clone RP11-348A20, WORKING DRAFT SEQUENCE, 23 unordered pieces. AC018803
   Unpublished
   The sequence of Homo sapiens clone
  Waterston, R.H.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Homo sapiens
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Insert size: 159843; sum-of-contigs
  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
   NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
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   10088
   40850:
   1403:
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   contig
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of 5762
  of 4732
   of 2894
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  of 2766
   of 2098
   of 1685
  of 1636
  of 1403
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of 13911 bp in
  of 6667
  of 4880
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  of 6390
   of 5843
  of 4519
   of 5328
   of 4681
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  of 3969
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   unknown
  unknown
   unknown
   bp in
  bp in
   ďď
   ďď
  bp in
  dq
   ď
   ďq
   đđ
   þ
  ģ
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  bp in
   bp in
   bp in
   bp in
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  length
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Homo sapiens chromosome 11 clone RP11-348A20 map 11,
SEQUENCE, 18 unordered pieces.
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Mammalia; Eutheria; Primates;
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  Score 45.8; DB Pred. No. 0.002;
    Nusbaum, C. and Lander, E
   Mismatches
                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
   37;
   2;
   2297 others
   Length 162043;
   Indels
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FEATURES

HTG 21-JUL-2001 WORKING DRAFT

0;

Gaps

0

145827

source

```
JOURNAL
REFERENCE
AUTHORS
   COMMENT
   JOURNAL
   Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
AL Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 20, 2001 this sequence version replaced gi:14210549.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://frn.gronme.usabing.com/papeatMasker.
   Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Pitzhugh, W., Gage, D., Galagan, J., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Granders, T., Johnson, R., Landers, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Thomas, R., Landers, R., Landers, R., Landers, T., Thomas, R., Landers,  http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
  Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrin,J., Meneus,L., Mihova,T., Mlenga,V.,
   Unpublished
  Homo sapiens chromosome 11, clone RP11-348A20
  NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
   (bases 1 to 166076)
   Quality coverage: 8.2 in Q20 bases; agarose-fp Quality coverage: 8.2 in Q20 bases; sum-of-contigs
  Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 160051 bases at least Q40
Consensus quality: 162378 bases at least Q30
Consensus quality: 162389 bases at least Q20
Consensus quality: 163489 bases at least Q20
  Insert size: 164000; agarose-fp
Insert size: 164376; sum-of-contigs
   Sequencing vector: Plasmid; n,
  Center clone name: 348_A_20
   Contact: sequence_submissions@genome.wi.mit.edu
  Web site: http://www-seq.wi.mit.edu
  Center code: WIBR
   Center: Whitehead Institute/ MIT Center for Genome Research
  11857 11956:
11957 136
   10151 10250:
10251 118
  5709 5808:
5809 68
   13686 13785:
   8334 8433:
8434 101
  6865 6964:
6965 83
16972:
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5808: gap of 100 bp
6864: contig of 1056 bp in length
6964: gap of 100 bp
833: contig of 1359 bp in length
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10150: contig of 1717 bp in length
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11856: contig of 1606 bp in length
11956: gap of 100 bp
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11956: gap of 100 bp
11956: contig of 1729 bp in length
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  Anderson, S.,
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  misc_feature
  misc_feature
   misc_feature
  misc_feature
   source
   47135
   102251 102350: gap of 100 bp
102351 114827: contrig of 12477 bp in length
114828 114927: gap of 100 bp
114928 129464: contrig of 14537 bp in length
129465 129564: gap of 100 bp
129565 163190: contrig of 33626 bp in length
   102251 102350:
102351 114827
   163191 163290: gap of 163291 166076: cont
  56432 56531: gap of 100 bp
56532 64713: contig of 8182 bp in length
64814 64813: gap of 100 bp
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  16973 20146: contig of 3174 bp in length
20147 20246: gap of 100 bp
20247 53285: contig of 33039 bp in length
53286 53385: gap of 100 bp
53386 56431: contig of 3046 bp in length
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   87627 87726:
   72677 72776:
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  .13685
   .72676
   .166076
  .114827
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   contig of 2786
   ap of 100 bp
contig of 33626 bp in length
  100 bp
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```
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AUTHORS
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   SOURCE
  DEFINITION
  AC090804
   KEYWORDS
   VERSION
   ACCESSION
   TITLE
   ORGANISM
  Matches
  JOURNAL
  JOURNAL
   TITLE
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   15 atggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctg 74
  Local
  Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Johnes, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McCwan, P., McKernan, K., Marquis, N., Mattheys, C., McCarthy, M., McNewan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Fieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roya, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roya, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
  2 (bases 1 to 166496)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barran,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
   Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Fu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
   Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 27, 2001 this sequence version replaced gi:13270673.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
  Homo sapiens chromosome 11, clone RP11-258P13
   1 (bases 1 to 166496)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
   Homo sapiens chromosome 11 clone RP11-258P13 map 11,
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Homo sapiens
  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
   AC090804.2 GI:14210577
  SEQUENCE, 7 unordered pieces.
  AC090804
  Similarity
Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 163137 bases at least Q40 Consensus quality: 16434 bases at least Q20 Consensus quality: 164323 bases at least Q20
   Center project Information
  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
  Center clone name: 258_P_13
   Contact: sequence_submissions@genome.wi.mit.edu
  Web site: http://www-seq.wi.mit.edu
  Conservative
   Eutheria;
   38.2%;
   - Genome Center
   Primates; Catarrhini; Hominidae; Homo.
   Score 45.8; DB 2;
Pred. No. 0.002;
0; Mismatches 37;
  166496 bp
  Length 166076;
  Indels
  of reads
   HTG 19-JAN-2002
  0;
   WORKING DRAFT
   Gaps
  0,
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LOCUS
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Best Local
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   15 atggcatagaaagagcaggaccttggggagcaagaatatctaagtttaattcctgactctg 74
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AL133413
   Similarity
   runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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   arbitrary. Gaps between the contigs are represented as
  47782 a
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Insert size: 165896; sum-of-contigs
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Quality coverage: 8.4 in Q20 bases;
  118291 118390: gap of 100 bp
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64550 64649: gap of 100 bp
6457 73576: contig of 8927 bp in length
73577 73676: gap of 100 bp
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  61086.
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  .60985
  35863 g 43706 t
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157790 bp
   Mismatches
  DNA
   in length
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   agarose-fp
sum-of-contigs
  612 others
   Indels
  linear
    PRI 03-JAN-2002
   0; Gaps
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QΥ

0;

DEFINITION

Human DNA sequence from clone

RP11-54K22 on chromosome

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FEATURES
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SOURCE
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VERSION
  REFERENCE
   AUTHORS
TITLE
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  JOURNAL
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  misc_feature
  source
  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EM:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; W:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human hard sequence that the sequence was generated from part of bacterial clone contigs of human hard sequence was generated from part of bacterial clone contigs of human hard sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was generated from part of bacterial clone contigs of human human sequence was 
   together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
  chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-54K22 is from the library RPCI-11.1 constructed at the Roswell
  Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
  On Feb 11, 2000 this sequence version replaced gi:6966862. During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations
  9q34.11-34.2. Contains an MTND3 (mitochondrial NADH dehydrogenase 3) pseudogene, STSs and GSSs, complete sequence.
  VECTOR: pBACe3
   Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
  feature key.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 157790)
   Homo sapiens
   AL133413.5 GI:6967346
   ттоуа, в
  sequence is the entire insert of clone RP11-54K22
   Submission
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match: STS: Em:G53956"
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   /note="MIR repeat: matches 2. .120 of consensus"
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          repeat: matches 6140.
   matches 14.
   matches 209. .253 of consensus"
   Em: B86764"
   .162
  .192 of consensus"
          . 6288
   of consensus"
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/note="LIME3A repeat: matches 5285. .5895 of consensus"
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3800. .3904
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4484. .4887
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  /note="L1PA3
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   note="AluSx repeat: matches 1.
   note="match:
   note="match: GSS: Em:AQ177739"
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  note="MER1B repeat: matches 1. .336 of consensus"
  'note="LTR16C repeat: matches 208.
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   /note="MLT1C repeat: matches 268. .421 of consensus"
  'note="match: GSS: Em:AQ580536"
   'note="LTR38 repeat: matches 1.
  note="MER2
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   /note="MER2 repeat; matches 89. .335 of consensus"
   /note="L1MD repeat: matches -1. .1597 of consensus"
10112. .10338
  /note="TIGGER2 repeat: matches 1. .45 of consensus"
   4908. .5087

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  .21546
   LIME1 repeat: matches 4904. .5252 of consensus 25670
  EKZ repeat: matches 24.
13179
   10650
                              repeat: matches 1781.
   repeat: matches 6239.
  repeat: matches 5547.
   GSS:
   GSS:
   GSS: Em: AQ476746"
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  5821.
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consensus"

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of consensus"

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   AGAAGATGTGGACAGAGCACAGTAAGAGTGTATGCTTTGGAGCCAGGCTTACTCAGTTTG 84208
Human DNA sequence from clone RP1-68P15 Contains ESTs, STSs and GSSs, complete AL390768.1 GI:9581737
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   20943. .2/004
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   /note="L2 repeat: matches 2267. .2464 of 26431. .26502
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  /note="MER47A repeat: matches 2.
complement(39672. .40087)
  /note="match: 44585. .44633
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  /note="MIR repeat: matches 12.
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35808. .36027
  /note="LIMC1 repeat: matches 6164 .6322 of consensus"
   'note="AluSx repeat: matches 7. .296 of consensus"
  note="L2 repeat: matches 2378. .
   note="match: GSS: Em:AQ400397"
   'note="match: GSS: Em:AQ545486"
  note="match: GSS:
   /note="match: GSS: Em:AQ613598"
   note="match: GSS: Em:AQ432498"
  note="MSTA repeat: matches 1. .426 of consensus"
   note="MER49"
   note="MER49 repeat: matches 575., .923 of consensus"
  37.3%;
   .34891
  .35247
   .30436
  .45009
  MEK49 repeat: matches 14.
  .41770
  .36288
   .32662
   .40739
   .44980
  ER49 repeat: matches 486. | .549 of consensus"
12287
   repeat: matches 2177. .2750 of consensus"
   copies 2 mer gt 84% conserved"
  0,
  Score 44.8; DB Pred. No. 0.004;
  GSS: Em:AQ203945"
  57449 bp
  Mismatches
  Em: AQ123877"
  Em: AQ436712"
   DB 9;
  DNA
   42; | Indels
  .235 of consensus"
   on chromosome 11p13-14.
   sequence
  .2750
  366 of consensus
   '127 of consensus"
  2696 of
  linear
   Length 157790;
  of
  of
  consensus"
  PRI 27-SEP-2000
  0;
  Gaps
   REFERENCE
AUTHORS
   COMMENT
  SOURCE
  FEATURES
  KEYWORDS
   TITLE
   ORGANISM
  JOURNAL
  repeat_region
   misc_feature
   misc_feature
  source
  repeat_region
   repeat_region
  repeat_region
    repeat_region
   repeat_region
  repeat_region
   repeat_region
  repeat_region
   repeat_region
   repeat_region
  requests: clonerequest@sanger.ac.uk During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
   i (bases 1 to 57449)
   RP1-68P15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP5-1137017 is at 57350 in this
   http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-68P15 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see
   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
  annotated human repeat sequence elements (e.g. Alu). Whe sequence is ambiguous, there is an annotation using the
  This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
  CB10 1SA,
  Submitted
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Homo sapiens
   sequence
   only a small overlap as described above.
   Direct Submission
   sequence. The true right end of clone XX-SRL9A13 is at 100 in this
  feature key.
   MPORTANT: This sequence is not the entire insert of clone
  nttp://bacpac.med.buffalo.edu/
   PCYPAC2
  (15-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
   /note="AluJb repeat: matches 82. 4502. .4569
   /note="AluJb repeat: matches 1. .301 of consensus"
3516. .4011
   2858.
  2426.
  1166.
  /note="AluSq repeat: matches 1. .310 of consensus"
   /map="p13-14.2"
/clone="RP1-68P15"
   /db_xref="taxon:9606"
  Location/Qualifiers
  11168.
   /note="HAL1 repeat: matches 551.
  /note="MIR repeat: matches 5. .241 of consensus"
   /note="AluJo repeat: matches 121.
   'note="MER3 repeat: matches 2. .205 of consensus"
   note="match: GSS: Em:AQ244277"
  note="match: GSS: Em:AQ278896"
   clone_lib="RPCI-1"
  'Chromosome="11"
   organism="Homo sapiens"
                             /note="
   note="34 copies 2 mer ga 69% conserved"
   note="HAL1 repeat: matches 11. .135 of consensus"
  .57449
   . 634
   .10960
                           MLT1A2 repeat: matches 1.
  L1PA2 repeat: matches 395.
                               .114 of consensus"
  .303 of consensus"
   .1073 of consensus
   .287 of consensus
  .6141 of consensus"
   Where the
  'unsure'
```

8 В 8

```
repeat_region
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   complement(32984. .33714)

/note="match: GSS: Em:AQ377120"
33454. .33536

/note="LIMA10 repeat: matches 6240. .6319 of consensus"
33537. .34804
                                       /note="L1MA10 repeat: matches 6167. .6240 of consensus" 35046. .41168
  34805
   31947. .33134
/note="L2 repeat: matches 1366. .2713 of consensus"
   /note="MER1A repeat: matches 1.
31376. .31910
   /note="HSMAR2 repeat: matches 1. .1300 of consensus"
   /note="MLT2D repeat: matches 42. .553 of consensus"
  /note="AluSp repeat: matches 1.
complement(25341. .25695)
  /note="AluJb repeat: matches 1 . .309 of consensus" 14364 . .14376 /note="LiPA16 repeat: matches 6081 . .6093 of consensus" 14377 . .14687 /note="AluSx repeat: matches 1 . .301 of consensus" /note="AluSx repeat: matches 1 . .301 of consensus"
   /note="45 copies 2 mer ta 66% conserved" 25259. .25559
  14688. .15421
/note="L1PA16 repeat: matches 5329. .6081 of consensus"
15422. .15678
  /note="MLTIA2 repeat: matches 9. .374 of consensus 11771. .11884 /note="MLTIA2-internal repeat: matches 1. .113 of consensus"
   /note="match: GSS: Em:B40764"
26535. .26614
   /note="MER7A repeat: matches 1. .292 of consensus"
24400. .24489
  /note="match: GSS: Em:B03931"
23411. .23714
   /note="L1PA2 repeat: matches 4493. .6146
21580. .21989
  /note="AluSg repeat: matches 1. .293 of consensus"
  /note="AluSp repeat: matches 1. .185 of consensus"
18784. .19104
  17079. .17509

/note="match: GSS: Em:AQ079766"

17089. .17465

/note="TIGGER1 repeat: matches 1950. .2359 of consensus"
  16040.
   /note="AluSx repeat: matches 8. .289 of consensus" 15679. .16039
   /note="MLT1A2 repeat: matches 13. .114 of consensus"
11392. .11770
   /note="AluSx repeat: matches 1 ..302 of consensus"
24111 ..24395
   14057
   16040. .16351

Note="Alux repeat: matches 1. .312 of consensus"
   /note="L1PA16 repeat: matches 6093. .6157 of consensus"
   'note="TIGGER1 repeat: matches 771. .1964 of consensus'
  /note="AluJo repeat: matches 1. .289 of consensus"
   /note="L1ME1 repeat: matches 5964. .6164 of consensus"
   .14363
   .13985
  .12436
               repeat: matches 2. .6144 of consensus'
   .527 of consensus"
   .299 of
   .374 of consensus"
   consensus"
   of consensus"
```

SOURCE ORGANISM

Homo sapiens

KEYWORDS VERSION ACCESSION DEFINITION

HTG; HTGS\_PHASE1; HTGS\_DRAFT. AL136384.8 GI:9542701

```
RESULT 13
AL136384/c
  QУ
  В
  Matches
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Best Local Similarity
  3061 AAGAGGATGAGCTACAGAGCAAGACTTTCCAAACTCAAGTCCTGGGTCTGCTACTTAATT 3002
  3001 ACTITGCGACCTTGGACAAGTTAATTAACCTTTGT 2967
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  repeat_region
  repeat_region
  repeat_region
  repeat_region
  misc_feature
  misc_feature
  repeat_region
  repeat_region
  repeat_region
   repeat_region
   85 actaaccatctttgccaatgttgcttaagcttttt 119
   172516 bp DNA linear HTG 26-JUL-2000 Homo sapiens chromosome 11 clone RP1-68P15 map p13-14.2, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
AL136384
  Conservative
  /note="L1 rer-
46547
  /note="L2 repeat: matches 2042. .2191 of consensus" 51492. .51812 /note="Alura8 repeat: matches 1. .309 of consensus"
   51044. .51354
/note="AluYa8 repeat: matches 1. .309 of consensus"
51364. .51491
  /note="LIME1 repeat: matches 5833. .6099 of consensus"
49539. .49823
   48839. .49096
/note="LLME1 repeat: matches 5569. .5834 of consensus"
49147. .49207
  /note="L1ME1 repeat: matches 4648. .5569 of consensus"
48530. .48838
  /note="Aluxb8 repeat: matches 1, 46098, .46235
  /note="match: GSS: Em:AQ789501" 45717. .45996
   /note="LIMEc repeat: matches 1580. .2001 of consensus" 41590. .41864
/note="Alux repeat: matches 30. .304 of consensus"
  /note="MSTA re
47708. .48529
   44654. .44851
/note="match: GSS: Em:AQ451420"
  50862. .50911
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   46547. .46703
/note="L1ME1 repeat: matches 3983. .4145 of consensus"
47012. .47330
/note="L1ME1 repeat: matches 4320. .4648 of consensus"
  /note="AluJb repeat: matches 6. .287 of consensus"
   /note="MER2 repeat: matches 25. .84 of consensus"
   /note="AluSx repeat: matches 3. .311 of consensus"
   /note="L1M4 repeat: matches 3517. .3671 of consensus"
   /note="FLAM_C repeat: matches 1.
   /note="43 copies 2 mer aa 62% conserved"
  /note="LIMEc repeat: matches 283.
43772. .43857
   36.5%;
  .51086
  .49884
  .47707
  .49538
  .44695
   .43166
   repeat: matches 3572. .3761 of consensus"
  Score 43.8; DB 9; Length 57449;
Pred. No. 0.0084;
0; Mismatches 32; Indels 0;
   repeat: matches 1. .426 of consensus"
  repeat: matches 6099. .6155 of consensus"
   .297 of consensus"
   .133 of
   .1580 of
   consensus"
  Gaps
  0;
```

```
FEATURES
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   REFERENCE
  밁
  밁
  ORIGIN
  BASE COUNT
DEFINITION
  HS37J18/c
  RESULT
   AUTHORS
TITLE
   JOURNAL
  Matches
  Query Match
  97986 AAGAGGATGAGCTACAGAGCAAGACTTTCCAAACTCAAGTCCTGGGTCTGCTACTTAATT 97927
  97926 ACTITGCGACCTTGGACAAGTTAATTAACCTTTGT 97892
  misc_feature
  misc_feature
   source
  85 actaaccatctttgccaatgttgcttaagcttttt 119
  Local Similarity
  Chemistry: Dye-terminator ABI; 0% of reads Chemistry: Dye-terminator Big Dye; 99% of reads Consensus quality: 155580 bases at least 040 Consensus quality: 155880 bases at least 030 Consensus quality: 155942 bases at least 020
   Submitted (25-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 153, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 27, 2000 this sequence version replaced gi:9501161.
  63;
  Insert size: 172416; sum-of-contigs
Insert size: 150759; 12.6% error; agarose-fp
Quality coverage: 0.00x in Q20 bases; sum-of-contigs Quality
coverage: 0.00x in Q20 bases; agarose-fp
  Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads
   1 (bases 1 to 172516)
Hall, R.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Center project name: dJ68P1
   Contact: humquery@sanger.ac.uk
   Web site:
   Center code:
   Center: Sanger Centre
  Direct Submission
Human DNA sequence from clone
                      HS37J18
  56528
  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
  NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
  be preserved
  16301 16400:
16401 17251
  Conservative
  1 15400: gap of 100 bp 1 172516: contig of 156116 bp in length.
  /chromosome="11"
/map="p13-14.2"
/clone="RP1-68P15"
  /note="assembly_fragment:02915.0"
30286 c 30207 g 55395 t 10
   1. .16300
  /organism="Homo sapiens"
   1. .172516
   http://www.sanger.ac.uk
  /clone_lib="RPCI-1"
  /db_xref="taxon:9606"
   SS
  36.5%;
66.3%;
  16300: contig of 16300 bp in length
   Summary Statistics
   Genome Center
   Project
  0,
  Score 43.8; DB 2
Pred. No. 0.0078;
                      131427 bp
   Information
  Mismatches
  37J18 on chromosome 1p36.2-36.3.
                      DNA
  DB 2;
  32;
  100 others
  Indels
  Length 172516;
                      linear
                   PRI 23-NOV-1999
  0;
  Gaps
  0;
   VERSION
KEYWORDS
  COMMENT
   REFERENCE
   SOURCE
   FEATURES
  ACCESSION
```

```
AUTHORS
TITLE
  JOURNAL
  ORGANISM
   source
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   repeat_region
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  repeat_region
   repeat_region
                         repeat_region
   repeat_region
  repeat_region
   repeat_region
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  repeat_region
   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.

This sequence is the entire insert of clone 37J18. This sequence has been finished according to sequence map criteria as follows. A attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
   Submitted (02-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequestesanger.ac.uk on Dec 2, 1998 this sequence version replaced gi:3925562.
   http://www.sanger.ac.uk/HGP/Chr1
37J18 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
  Grafham, D.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 131427)
  Homo sapiens
   HTG
   Z98747.1 GI:3947813
  Contains a putative novel gene, ESTs and GSSs, complete sequence. z98747
  human chromosome 1, constructed by the Sanger Centa
Mapping Group. Further information can be found at
  This sequence was generated from part of bacterial clone contigs human chromosome 1, constructed by the Sanger Centre Chromosome
  eature key
   Submission
  5386.
  4051
  2191.
   563.
   3603
   /clone_lib="RPCI-1"
   /map="p36.2-36.3"
/clone="RP1-37J18"
  /db_xref="taxon:9606"
/chromosome="1"
   /organism="Homo sapiens"
   Location/Qualifiers
  /note="
   /note="
  /note="2]
  /note="4 copies 24 mer 81% conserved"
  /note="
/note="MLT1B repeat: matches 1. .381 of consensus"
   /note="MIR repeat: matches 53. .144 of consensus"
  note="1
  /note="14 copies 20 mer 58% conserved"
  /note="AluSx repeat: matches 1. .294 of consensus"
  note="MIR repeat: matches 141. .210 of consensus"
  note="28 copies 2 mer tt 79% conserved"
   e="212 copies 3 mer cac 80% conserved" .1168
   .1156
  .3899
   "9 copies 66 mer 82% conserved"
.1613
  MLT1J repeat: matches 25.
  LlMA4A repeat: matches 6071. .6295 of consensus"
   .41 copies 2 mer cc 57% conserved"
   copies 37 mer 79% conserved"
  copies 24 mer 79% conserved"
   .508 of consensus"
  with
  0
t
   Α'n
```

```
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  19100. 19140
/note="MLTIE repeat: matches 72. .112 of consensus"
19854. .19922
  /note="5 copies 70 mer 93% conserved" 15459. .15668 /note="6 copies 35 mer 91% conserved" 15681. .15827
   /note="9 ccr
   /note="Forced join in tandem repeat; gap clones and PAC PCR to be 1-200bp"
   /note="7 cc 1474°
/note="MIR repeat: matches 87. .163 of consensus"
  /note="L2 repeat: matches 2413.
16974. .17269
  /note="MLT1D repeat: matches 1.
16463. .16529
   7430.
   6180. .6476

/note="LIMB7 repeat: matches 5847. .6143 of consensus"

6535. .6856
   5862. .6059
/note="L1MB7 repeat: matches 5654. .5862 of consensus"
6060. .6116
/note="Charliel repeat: matches 2407. .2463 of consensus"
  'note="L2 repeat: matches 2538. .2685 of consensus"
  note="MLT1E repeat: matches 249.
  'note="MER77 repeat: matches 5.
   nore="5 copies 91 mer 93% conserved"
[5124._.15428
  /note="AluSg repeat: matches 1..308 of consensus"
8477..8512
/note="12 copies 3 mer taa 83% conserved"
   'note="Tandem repeat; poor quality data
   'note="7 copies 70 mer 91% conserved"
14748. 15237
'note="114 copies 35 mer 90% conserved"
   'note-"MER31B repeat: matches 1. .543 of cons
(4734. .15230
"note="71 copies 7 mer gctgtgt 90% conserved"
  3961. .9108
/note="AluSx repeat: matches 132. .289 of consensus"
10990. .11231
  3647. .8960 "Alusq repeat: matches 1. .313 of consensus"
  3517. .8646
/note="Alusx repeat: matches 6. .132 of consensus"
   7784. .7911
/note="11194 repeat: matches 5288. .5414 of consensus"
   7430. .7481
/note="13 copies 4 mer catt 77% conserved"
   6535. .6856
/note="Charliel repeat: matches 2146. .2458
   note="5 copies 91 mer 92% conserved"
   5210. .15320
note="3 copies 37 mer 78% conserved"
5230. .15684
  note="match: GSS AQ203924"
4049. .14489
  'note="AluSx repeat: matches 8. .309 of consensus"
  .1467. .11756
'note="L2 repeat: matches 2359.
.2285. .12575
  'note="MIR repeat: matches 2. .249 of consensus"
.1467. .11756
   'note="L1M4 repeat: matches 5086. .5272 of consensus"
  6 copies 4 mer aatg 100% conserved".19007
  .16348
  .18555
   .15661
  .12800
   .15209
   copies 3 mer tga 93% conserved"
  .2474 of consensus
  .504 of consensus"
  .2625 of consensus
  .331 of consensus"
  .562 of consensus"
   over region"
   sized
  consensus"
   of consensus"
   bу
   puc
```

```
RESULT 15
AC064798
   B
  В
   Matches
  81037 CTAGCTATGTGGCTTTGGGCAAATTACTCAACCTCTCT 81000
  81097 AGGTAGGGCATGGATTTGGGAGCCAGAAAGCCCAGGTTCAAATCCTGACTCTGCCACTTA 81038
   repeat_region
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  repeat_region
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  repeat_region
  repeat_region
   repeat_region
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  Local Si 64;
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  repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
  82 ttaactaaccatctttgccaatgttgcttaagcttttt 119
  22 agaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctattta 81
Homo sapiens chromosome I clone SEQUENCE, 26 unordered pieces. ACC64798 GI:7885063
   a 36.3%;
Similarity 65.3%;
54; Conservative
   29048. 29167
/note="5 copies" 16 n
29057
  /note="L1ME3 repeat: matches 5937. .6164
30493. .30540
/note="3 copies 16 mer 88% conserved"
  /note="7 cor
29692
  /note="L1PA5 repeat: matches 5943. .6042 of 29872. .29911
  /.uuce="5 copies 24 mer 70% conserved" 29057. .29147 //note="7 copies 1"
  /note="7 copies 13 mer 69% conserved"
29072. .29151
/note="20 copies 4 mer aaat 66% conserved"
29200. .29504
  /note="2 copies 66 mer 83% conserved"
29040, .29119
/note="5 copies 16 mer 73% conserved"
   19928. .19988
/note="MER53 repeat: matches 128.
20239. .20321
  /note="20 copies 2 mer aa 80% conserved"
  complement(25095
   22083. .22359
/note="L2 repeat: matches 2416.
  /note="2 copies 70 mer 84% conserved"
29037. .29168
   26856. .27160

"Note="Allusg repeat: matches 1.

27460. .27770

Prote="Allusg repeat: matches 1.
   /note="match: GSS AQ192529"
26500. .26778
  /note="MER70A repeat: matches 127. .545 of consensus"
complement(25095. .25545)
   note="18 copies 2 mer ta 81% conserved"
   /note="AluJb_repeat: matches 1.
  /note="MMR53 repeat: matches 94. .182 of consensus"
20256. .20337
   note="AluSq repeat: matches 1. .304 of
   note="Alusx
  note="MIR repeat: matches 13. .126 of consensus"
  /note="L2 repeat: matches 2638.
   /note="MER63A repeat: matches 42. .208 of consensus"
   /note="MER53 repeat: matches 1. .89 of consensus"
  "7 copies 16 mer 69% conserved" .29725
  .29175
  . 29865
  . 28292
  0; Mismatches
   Score 43.6; DB 9;
Pred. No. 0.0091;
   repeat: matches 21.
   34;
  .2710 of consensus"
   .311 of consensus"
   .301 of consensus"
   Length 131427;
   .305 of
  .2747 of
   . 297
   Indels
   .187 of consensus"
   of.
   consensus"
   of.
   consensus"
   consensus"
   consensus"
   0;
  consensus"
  consensus"
   0;
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ACCESSION VERSION

DEFINITION

RP11-182C20 map 1, DNA

linear

HTG 17-MAY-2000 WORKING DRAFT

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REFERENCE
AUTHORS
  COMMENT
   SOURCE
  REFERENCE
  ORGANISM
   JOURNAL
   TITLE
   AUTHORS
  JOURNAL
  Howland, J.C., Iliev.I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Voassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zimmer, A. and Zody, M.
  Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 17, 2000 this sequence version replaced gi:7637293.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedd, F., Bouguslawkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dewar, K., Diaz, J.S., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Cooke, P., Dewar, K., Diaz, J.S., Cooke, P., Dewar, K., Dewar, K., Diaz, J.S., Cooke, P., Dewar, K., De
   Grand-Pierre,N., Grant,G., Hagos,B., Heaford, Howland,J.C., Illev,I., Johnson,R., Jones,C.,
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  Homo sapiens
  Galagan, J., Gardyna, S.,
  Dodge,S., Domino,M., Doyle,M.,
   Unpublished
   Homo sapiens chromosome 1, clone RP11-182C20
  HTG; HTGS_PHASE1; HTGS_DRAFT
   NOTE: This is a 'working draft' sequence, It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
  as soon as it is available and the accession number will be preserved. \begin{tabular}{c} \end{tabular}
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  (bases 1 to 157185)
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Consensus quality: 145137 bases at least Q40
Consensus quality: 150882 bases at least Q30
Consensus quality: 153238 bases at least Q20
   Seguencing vector: M13; M77815;
   Center project name: L759
Center clone name: 182_C
  Contact: sequence_submissions@genome.wi.mit.edu
   Insert size: 157000; agarose-fp
Insert size: 154685; sum-of-contigs
   Web site: http://www-seq.wi.mit.edu
  Center code: WIBR
  Center: Whitehead
  1409 1508: gap of
1509 2661: cor
  2662 2761: gap of
2762 4282: con
       4382: gap (
   Eutheria;
   ---- Genome Center
  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   1408: contig of 1408 bp in
   p of 100 bp
contig of 1153 l
p of 100 bp
contig of 1521 b
               contig
   Institute/ MIT Center for Genome Research
  Ginde, S., Goyette, M., Graham, L.,
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of 1763
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bp_in
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  bp in
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   length
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  misc_feature
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  120545 120644: gap of 100 bp
120645 137261: contig of 16617 bp in length
137262 137361: gap of 100 bp
137362 157185: contig of 19824 bp in length
   108185 108284: gap of 108285 120544: cont
  10647 10746: gap of 100 bp
10747 13916: contig of 3170 bp in length
13917 14016: gap of 100 bp
14017 16335: contig of 2319 bp in length
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   78518 78617:
  65413
  51543
  44607
  39516
   39416
  36498
  36398
  28318
   23959
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6246 8:
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39415: contig of 2918 bp in length

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44606: contig of 5091 bp in length
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  36397: ~
  23858:
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12: gap of 100 bp
10646: contig of 2234 bp in
   06: gap of 51542: cont
  32600:
  5: gap of
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contig of 4283 bp in length
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contig of 2845 bp in
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of 2067 bp in
100 bp
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2002, 18:23:45
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Search completed: September Job time: 28924 sec

0,:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Database
  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
  Total number of hits satisfying chosen parameters:
   Scoring table:
  Title:
Perfect score:
  Run on:
  OM nucleic -
  Searched:
   nucleic search, using sw model
  US-09-834-291-1_COPY_1266_1285
20
   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
   September
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em_gss_inv:*
em_gss_pln:*
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em_estpl:*
  em_esthum:
  gb_est2:*
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   gb_gss:*
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(c) 1993 - 2000 Compugen Ltd.
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   (without | alignments)
31.898 Million cell updates/sec
   Search time 8462.63 Seconds
  27472414
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | 17                 | 16                 | 15                | c 14               | c 13               | 12                | 11                 | c 10               | o<br>9             | 80                | 7                 | 6                  | ი<br>5             | 4                  | ი<br>ა             | 2                  | 1                  | Result<br>No.            |
|---|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------------|
|   | 16.8               | 16.8               | 16.8              | 16.8               | 16.8               | 16.8              |                    | 16.8               | 16.8               | 16.8              | 16.8              | 17.4               | 17.4               | 17.4               | 17.4               | 18.4               | 18.4               | Score                    |
|   | 84.0               | 84.0               | 84.0              | 84.0               | 84.0               | 84.0              | 84.0               | 84.0               | 84.0               | 84.0              | 84.0              | 87.0               | 87.0               | 87.0               | 87.0               | 92.0               | 92.0               | Query<br>Match 1         |
|   | 831                | 785                | 673               | 576                | 540                | 442               | 424                | 409                | 374                | 331               | 320               | 1101               | 1028               | 714                | 622                | 527                | 256                | Query<br>Match Length DB |
|   | 10                 | 12                 | 9                 | 12                 | 12                 | ဖ                 | 12                 | 12                 | 12                 | 9                 | ဖ                 | 12                 | 12                 | 12                 | 9                  | 10                 | 9                  | - BB                     |
|   | BE704507           | вн116550           | AV834315          | AZ483186           | в88004             | AL509860          | вн400996           | AQ475625           | AZ110509           | BB559660          | BB066589          | CNS0024V           | CNS010LK           | AZ966012           | AW943206           | BG267668           | AI629829           | ID                       |
| _ | _                  |                    | -                 | _                  | -                  | _                 |                    | _                  |                    |                   | -                 |                    |                    |                    | _                  |                    |                    | 1<br>1<br>1<br>1<br>1    |
|   | BE704507 Sc01_05h0 | BH116550 RPCI-24-2 | AV834315 AV834315 | AZ483186 1M0308N08 | B88004 RPCI11-16C2 | AL509860 AL509860 | BH400996 AG-ND-124 | AQ475625 CITBI-E1- | AZ110509 RPCI-23-4 | BB559660 BB559660 | BB066589 BB066589 | AL062157 Drosophil | AL099122 Drosophil | AZ966012 2M0236018 | AW943206 LD33880.3 | BG267668 1000135F1 | A1629829 486039F12 | Description              |

| 000                                                                                 | 0 0                                                                | 0                                          | 0 (                                                            | o o                                                                                                     | α α α                                                                                                                          |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|
| 42<br>43<br>45                                                                      | 36<br>37<br>38<br>40<br>41                                         | 33<br>34<br>35                             | 29<br>30<br>31                                                 | 24<br>25<br>26<br>27                                                                                    | 18<br>19<br>20<br>21<br>22<br>23                                                                                               |
| 15.8<br>15.8<br>15.8                                                                | 15.8<br>8 8 8 8                                                    | 15.8<br>15.8                               | 15.8<br>15.8                                                   | 15.8<br>15.8<br>15.8                                                                                    | 16.4<br>16.4<br>16.4<br>15.8                                                                                                   |
|                                                                                     | 79.0<br>79.0<br>79.0<br>79.0                                       | 79.0<br>79.0<br>79.0                       | 79.0<br>79.0<br>79.0                                           | 79.0<br>79.0<br>79.0<br>79.0                                                                            | 82.0<br>82.0<br>82.0<br>79.0                                                                                                   |
| 493<br>495<br>497<br>499                                                            | 446<br>459<br>469<br>486<br>493                                    | 416<br>418<br>433<br>442                   | 378<br>385<br>403                                              | 328<br>330<br>341<br>368                                                                                | 269<br>407<br>812<br>849<br>208<br>287                                                                                         |
| 12<br>10<br>12<br>9                                                                 | 10<br>10<br>12<br>12<br>12                                         | 9<br>12<br>12                              | 12                                                             | 10<br>10<br>10                                                                                          | 9<br>12<br>10<br>10                                                                                                            |
| AQ304517<br>N29129<br>AQ880539<br>AA401233                                          | AQ436731<br>BF413605<br>BF413606<br>B65834<br>AZ695007<br>AQ205575 | BE120640<br>AZ445420<br>AQ716681<br>N41676 | B27343<br>AW802137<br>AQ147024                                 | AU097685<br>BF331881<br>AV64599<br>BH041588<br>T87445                                                   | AV016820<br>AQ814525<br>BH268838<br>BG445507<br>AZ509241<br>Z28847                                                             |
| AQ304517 HS_3138_B<br>N29129 yx47e08.r1<br>AQ880539 HS_5045_B<br>AA401233 zv63e02.r | H                                                                  | UI-R-CA(<br>1M0241N<br>HS_5463<br>w90e07.j | B27343 T5D14TR TAM<br>AW802137 IL5-UM007<br>AQ147024 HS_2269_A | AU097685 AU097685<br>BF331881 QV1-BT063<br>AV645999 AV645999<br>BH041588 RPCI-24-3<br>T87445 yd89h05.r1 | AV016820 AV016820<br>AQ814525 HS_5265_A<br>BH368838 CH230-162<br>BG445507 GA_Ea002<br>AZ509241 IM0352P04<br>Z28847 HSBA5E061 S |

## ALIGNMENTS

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AUTHORS
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BASE COUNT
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  source
   Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
  University
Unpublished (1999)
Contact: Walbot V
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

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   Email: walbot@stanford.edu
Plate: 486039 row: F colu
   Zea mays.
  Department of Biological Sciences
   Maize ESTs from various cDNA libraries sequenced at Stanford
  Walbot, V
                 69
                 library."
a 70 c
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  Ŷ
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SOURCE
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BG267668
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AUTHORS
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  ORGANISM
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   Query Match
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les 19; Conserv
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   Email: walbot@stanford.edu
Plate: 1000135 row: F colu
Location/Qualifiers
  Stanford University
855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
   Walbot, V.
Maize ESTs from various
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  Fax: 650 725 8221
   Department of Biological Sciences
   Contact: Walbot V
   Unpublished (1999)
  University
  Zea mays
   BG267668.1 GI:12971808
EST.
   CDNA, mRNA sequence.
BG267668
   BG267668 527
1000135F11.x2 1000 - Unigene
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1e+02;
   DВ
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   9
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Contact: Robert B.
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and Wright,D.,Weiss,R.
   Mammalia; Eutheria; Rodentia; 1 (bases 1 to 714)
Dunn, D., Aoyagi, A., Barber, M.,
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University of Utah
University of Utah
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Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
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fruit fly.
   Plate: LD.338 row: G column: 8 High quality sequence stop: 423.
   genomic AE003636: Drosophila melanogaster genomic scaffold 142000013386055 section 29 of 63, complete sequence.: 03/12/2001
   Fax: 510 486 6798
  EDGF
Lawrence Berkeley National Lab
Carron Rd, Berkeley, CA 94720, USA
  Contact: Stapleton, M.
   BDGP/HHMI Drosophila EST Project
   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Lewis,S. and Rubin,G.M.
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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Pred. No. 3
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BASE COUNT
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  Email: ddunn@genetics.utah.edu
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Plate: 0236 row: 0 column: 18

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -

   Drosophila melanogaster genome survey sequence SP6 end of BAC BACN04I03 of DrosBAC library from Drosophila melanogaster (from BACN04I03)
   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyce Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
  Drosophila melanogaster
Eukaryota; Metazoa; Art
  GSS
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   Class: plasmid ends
   Seq primer: CGTTGTAAAACGACGGCCAGT
  AL099122.1 GI:5610733
   Direct Submission
   Genoscope
  fruit fly.
   Similarity
   (bases 1 to 1028)
  258
   801 585 5606
801 585 7177
   ligated to the blunt ends in high | molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  quality sequence stop: 714.
   Conservative
  genomic survey sequence.
   USA
  þ
  Biomedical Polymers Research Bldg.,
  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were
  (http://www.jax.org/resources/documents/dnares/). The DNA
   Laboratory Mouse DNA Resource
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  18;
   http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
  melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
  Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
  Drosophila melanogaster genome survey sequence T7 end of BAC BACR05E09 of RPCI-98 library from Drosophila melanogaster (fr
  Drosophila melanogaster
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   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  Genoscope.
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
  AL062157.1 GI:4940317
   fly), genomic survey sequence.
AL062157

    Web : www.genoscope.cns.fr)

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Laboratti Yoshihide Hayashizaki, Y., Takanaka, Y., Yananaka, I., Taboratti, Yoshihide Hayashizaki, Y., Yananaka, Y., Yan
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  Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303
  Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
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Carnincl.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
   P. Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
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, M., Muramatsu, M. and Hayashizaki, Y.
Onpublished (2000)
  1-7-22 Suehiro-cho, Tsurumi-ku,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
  BB559660 RIKEN full-length enriched, 2 days pregnant adult female DB559660 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330039011 3' similar to U49385 Mus musculus CTP synthetase homolog (CTPsH) mRNA, mRNA sequence.
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  Similarity
  Conservative
   99
  b
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Project of Genome Exploration Research Group in Riken
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
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   Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                                      Contact: Shaying Zhao
Department of Eukaryottic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
   Mouse BAC End Sequences from Library RPCI-23
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  and Fraser, C.M.
   house mouse.
  Similarity
  Please visit our web site (http://genome.ntc.riken.go.jp) for
   100
301 838 0200
301 838 0208
   Conservative
  prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research frough in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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  Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 471 row: O column: 7
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   Email: szhao@tigr.org
  Department of Eukaryotic Genomics
The Institute for Genomic Research
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Unpublished (1997)
Other_GSSs: CITBI-E1-2589J3.TF
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   Tel: 301 838 0200 Fax: 301 838 0208
   9712 Medical Center Dr., Rockville,
  Map Building
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  Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TICR). The BAC library was generated from A. gambiae PEST strain
DNA, All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
DNA title Content of the Conten
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
   partial digest
  Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftu Direct Submission of BAC-end sequences from Anopheles gambiae
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  Unpublished (2000)
Contact: Michalek W
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  Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: Ml3uni primer for 3'end.
  Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany
  Michalek, W., Weschke, W., Pleissner, K.-P.
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  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 576)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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  1M0308N08R Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGClM0308N08 R, DNA sequence. 
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  Class: BAC ends.
   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
  library availability, please contact Pieter de Jong (pieteer@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
   Clones are derived from the human BAC library RPCI-11. For BAC
   Contact: Mark Adams
   Unpublished (1998)
Other_GSSs: RPCI11-16C24.TP RPCI11-16C24.TVB
   Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
  Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
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Contact: Robert B.
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   AZ483186
                     Tel: 801 585 5606 Fax: 801 585 7177
   University of Utah
University of Utah
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  mdadams@tigr.org
ddunn@genetics.utah.edu
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밁 QΥ

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AUTHORS
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Contact: Kazuhiro Sato
Contact: Nostitute for Bioresources
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
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Hordeum vulgare subsp. vulgare
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   Email: kazsato@rib.okayama-u.ac.jp,
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database:http://www.shigen.nig.ac.jp/barley/Barley.html.
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   Triticeae; Hordeum.
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   adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored.
   Saisho,D.,
   adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."

91 c 113 g 206 t
  polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4
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 იიი
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  000
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 16.88
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Sequence 211812, A
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## ALIGNMENTS

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; GENERAL INFORMATION:
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SEQ ID NO 1262
LENGTH: 45121
           APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT ETLING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SED ID NOS: 1613
SCRUMBER OF SED ID NOS: 1613
  APPLICANT: MOTTIS, DAVID
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PRILING DATE: 2000-04-20
PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
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  APPLICANT: Wang, David G.
  CURRENT APPLICATION NUMBER: US/10/098,754
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/791539
PRIOR FILING DATE: 2001-02-22
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   APPLICANT: Ramachandran, Rakesh
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
FILE REFERENCE: ATX-001CN
   APPLICANT: Harrington, John J APPLICANT: Jackson, P. David
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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  US-10-098-754-11812; Application US/10098754; Sequence 11812; Application US/10098754
  Sequence 258417, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)...(1223)
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
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PRIOR FILING DATE: 1999-11-23
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GENERAL INFORMATION:
GENERAL INFORMATION: Javid G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-03-24
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PRIOR FILING DATE: 1999-11-23
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
   PRIOR EILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-08-09
  PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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APPLICANT: Yang, Fe1
APPLICANT: Yim, Kenneth
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From a CDNA Library of Fetal Liver-Spleen
FILE REFERENCE: 728CIP
CURRENT APPLICATION NUMBER: US/09/721,544
PRIOR APPLICATION NUMBER: 09/515,128
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PRIOR FILING DATE: 1999-08-09
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Dickson, Mark
   Smith, Benjamin
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  Kita, David
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  Engleman, Carrie
Faulkner, Brandy
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PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
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PRIOR FILLING DATE: 1999-09-28
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PRIOR FILLING DATE: 1999-08-09
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US-10-027-632-50683
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827,129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

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PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR ETLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR EILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR EILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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US-10-027-632-50683
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 1999-08-09
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
   GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-07-12
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PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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  Hepler, William T.
   Harlocker, Susan L.
   Mitcham, Jennifer L
   Sleath, Paul
  Jiangchun
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APPLICANT: Houghton, Raymond L.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Woshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-12
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
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; PRIOR APPLICATION NUMBER: DE 198 47 779.1
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; PRIOR FILING DATE: 1998-10-18
; PRIOR FILING DATE: 1998-10-16
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   APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
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APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
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CURRENT FILING DATE: 2001-08-21
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PRIOR FILING DATE: 1998-10-16
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 40
ORGANISM: Homo Sapiens
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   TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122 CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21
   APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-JAN-19:
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
   APPLICANT: Zhou, Tong
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
  APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, Willia
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
   STREET: P.O. B
CITY: Houston
STATE: Texas
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
  COUNTRY: US
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US-08-377-522-1
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INFORMATION FOR SEQ ID NO: 1:
  TELEFAX: (713) 777-6908 INFORMATION FOR SEQ ID NO:
   SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
   REFERENCE/DOCKET NUMBER: UO TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
  SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522C
  APPLICANT: Mountz et al.
TITLE OF INVENTION: Huma
   REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
  CLASSIFICATION: 435 PRIOR APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
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   CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: no
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  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
   TYPE: nucleic acid
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  REGISTRATION NUMBER:
  TYPE: nucleic acid
STRANDEDNESS: double-stranded
   NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
DEFENSE COCKET NUMBER: DE010
  FILING DATE:
   FILING DATE: January 20, 1995
  1 aaactacctaagagctatct 20
  STRANDEDNESS: single TOPOLOGY: linear
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  LENGTH:
   ADDRESSEE:
  20;
  77071
  Sertich, Gary J
  1608 bp
  E: Benjamin Aaron Adler, Ph.D., J.D. 8011 Candle Lane
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Best Local Similarity
   REFERENCE/DOCKET NUMBER: D59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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IMMEDIATE SOURCE:
LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
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DESCRIPTION:
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  SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
ORGANISM: human
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   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
  APPLICANT: Mountz et al.
  STREET: ...
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TTTY: Houston
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   ANTI-SENSE:
PUBLICATION INFORMATION:
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  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
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   TOPOLOGY:
   TYPE: nucleic acid STRANDEDNESS: double-stranded
   NAME: Benjamin Aaron Adler, Ph.D., REGISTRATION NUMBER: 35,423
  FILING DATE:
  APPLICATION NUMBER: US/08/377,522D
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   1608 bp
   8011 Candle Lane
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   Benjamin Aaron Adler, Ph.D., J.D
   January 20, 1995
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US-09-665-615B-94
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  Sequence 94, Application US/09665615B
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Myatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/09/640
PRIOR APPLICATION NUMBER: US/09/290,640
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PRIOR SEQ ID NOS: 179
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   Sequence 94, Application US/09802669
GENERAL INFORMATION:
APPLICANT: Mearcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Wyatt, Jacqueline
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   SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2000-09-18
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   PRIOR APPLICATION NUMBER: US 09/290,640 PRIOR FILING DATE: 1999-04-12
  APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
  TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-834-291-3
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
   Sequence 4, Application US/09834291 GENERAL INFORMATION:
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   Sequence 3, Application US/09834291 GENERAL INFORMATION:
  TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION UNMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION UNMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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  APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
   CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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  APPLICANT: Krammer, Peter APPLICANT: Muller-Schill
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PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
   APPLICANT: Engelhard, Eric
TITLE OF INVENTION: MOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71.17/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
   APPLICANT: Krammer, Peter APPLICANT: Muller-Schill APPLICANT: Oren, Moshe
   CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
   TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122
   PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 301
  APPLICANT: Morris, David APPLICANT: Engelhard, E
APPLICANT: Lalgudi, Raghunath, V.
  SOFTWARE: PatentIn version 3.1
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TELEFAX: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1327:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base --
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PRIOR FILING DATE: May 12, 1998
NUMBER OF SEQ ID NOS: 6550
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   APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN LEAF
FILE REFERENCE: PL-0013 US
CURRENT APPLICATION NUMBER: US/09/298,328A
CURRENT FILING DATE: 1999-04-21
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LOCATION: 159
OTHER INFORMATION: a, t,
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TELECOMMUNICATION INFORMATION:
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   ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
REGISTRATION NUMBER: 39,
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   209 AAACTACCTGAGAGCTATCT 190
   FILING DATE: H
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COMPUTER: IBM PC compatible
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; APPLICANT: Resphunath, Laigudi
; APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Ito, Laura Y.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN CALLUS
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US-60-085-147-1327
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| SOM PONTER PRESENTAL ELECTRONIC PONTER DESCRIPTION OF THE PROPERTY OF THE PROP |                                                  |
| 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 68. 13.6 70 Applicant Constant Con |                                                  |
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| 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                  |
| MANY R                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | JS-08-803<br>JS-08-803<br>JS-09-128<br>JS-08-374 |
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| N) *:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                  |
| Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Sequence<br>Sequence<br>Sequence<br>Sequence     |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                  |
| 2, Appli<br>23, Appl<br>23, Appl<br>79, Appl<br>168, Appli<br>1, Appli<br>1, Appli<br>1, Appli<br>1, Appli<br>14, Appli<br>14, Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                  |

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   Sequence 21, Application US/07744282C Patent No. 5521300 GENERAL INFORMATION:
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APPLICANT: Nietupski,
APPLICANT: Liu, Jing
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
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APPLICANT: Chen, Yen-Wen
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  Dow, Karen B.
   California
   Application US/09170996
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Nietupski, Raymond M.
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ATTORNEY/AGENT INFORMATION:
  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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   APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
NUMBER OF SEQUENCES: 127
   APPLICANT: Shah, Jyotsna S. APPLICANT: Nietupski, Raymond M. APPLICANT: Liu, Jing
  REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: GT
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  CORRESPONDENCE ADDRESS:
   TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
   FILING DATE: August 13, 1
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Fairell
   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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   STRANDEDNESS:
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  P.O. Box 999
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   E: Kevin M. Farrell, P.C. P.O. Box 999
   USA
  USA
  Kevin M. Farrell, P.C
   August 13, 1991
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CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Kevin M. Farrell
REGISTRATION NUMBER: 35,505
REFERENCE_PLOCKET NUMBER: GTR90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0528
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LENGTH: 126 base pairs
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STRANDEDNESS: double
   SOFTWARE: Patentin Reli
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APPLICATION NUMBER: US
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   APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
NUMBER OF SEQUENCES: 127
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  Conservative
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   DB 1;
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  US-08-484-105-3/c
  US-08-981-957D-12
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  SEQ ID NO 12
  Sequence 12, Application US/08981957D Patent No. 6312935
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  APPLICANT: KIY, THOMAS
APPLICANT: SCHULTZ, JOACHIM
TITLE OF INVENTION: CATHEPSIN-L, ITS PREPRO FORM AND THE CORRESPONDING
TITLE OF INVENTION: PROPERTIDE FROM CILIATES
FILE REFERENCE: 514426-3595
FILE REFERENCE: 514426-3595
   SOFTWARE:
  GENERAL
   TYPE: DNA ORGANISM: Paramecium tetraurelia
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                ATTORNEY/AGENT INFORMATION: NAME: Osman Ph.D., Richa
   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
  APPLICANT:
  TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
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  APPLICANT:
  STATE: Californ:   183 aactacatcagagctttct 201
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   FILING DATE
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   COUNTRY: USA
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   RINE, Jasper
FOSS, Margit
  Conservative
   GAVIN, Kimberly
  HERSKOWITZ, Ira
  McNALLY, Francis J
   KOBAYASHI, Ryuji
  BELL, Stephen P
   STILLMAN,
   LAURENSON, Patricia
  Joachim :
   71.0%;
84.2%;
                                Richard Aron
   Bruce
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TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
   Sequence 3, Application US/08484106 Patent No. 5614618
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
   APPLICANT:
APPLICANT:
  CORRESPONDENCE ADDRESS:
  APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
  APPLICANT:
APPLICANT:
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STATE: California
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  RINE, Jasper
FOSS, Margit
   BELL, Stephen P
KOBAYASHI, Ryuji
   LAURENSON, Patricia HERSKOWITZ, Ira
  MCNALLY, Francis J
   STILLMAN, Bruce
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PRIOR APPLICATION NUMBER: US 07/977,452
PTITING DATE: 17-NOV-1992
   REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
  FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl_
   FEATURE:
  SEQUENCE CHARACTERISTICS.
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION UNMBER: US 08/153,848
APPLICATION UNMBER: US 08/153,848
FILING DATE: 17-NOV-1993
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  SOFTWARE: PatentIn Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy
  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
   APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
  2539 ATCGACCTTAGAGCTATCT 2521
  TOPOLOGY: linear MOLECULE TYPE: cDN
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   FILING DATE:
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CITY: Chicago
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   COUNTRY:
   STATE:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
  NAME/KEY:
LOCATION:
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   (312) 474-0448
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6300 Sears Tower, 233 South Wacker Drive
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; LOCATION: US-09-299-843A-31
  US-09-088-337B-31/c
  ; SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-09-088-337B-31
   Sequence 31, Application US/09088337B Patent No. 6348574
GENERAL INFORMATION:
   ATTORNEY/AGENT INFORMATION:

NAME: NO. 6348574and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-6300

TELEFAX: (312) 474-6448

TELES: 25-3856

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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Best Local Similarity
Matches 16; Conserv
   2968 AGACTGCCAAAGAGCTATC 2950
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   APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
  APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   CORRESPONDENCE ADDRESS
   FEATURE:
  FEATURE:
  MOLECULE TYPE: CDNA
  16; Conservative
  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
  APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
  STATE: Illinois
  CITY: Chicago
   STREET: 6300 Sears Tower, 233 South Wacker Drive
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  COUNTRY: USA
   ADDRESSEE: Marshall, O'Toole, Gerstein,
  NAME/KEY:
LOCATION:
   NAME/KEY:
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94..1158
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7..80
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84.2%;
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  Score 14.2;
Pred. No. 76;
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Pred. No. 76;
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  DB
                                       DB 4;
  ω
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 ω,
Indels
   Murray &
  Ļength 3119;
                                     Length 3119;
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   δã
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Best Local Similarity
Watches 16; Conserve
  US-09-245-041-5
  US-09-245-041-5/c
   US-08-713-557B-30
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   GENERAL INFORMATION:
  Patent No.
   SEQ ID NO 5
   Sequence 5, Application US/09245041 Patent No. 6274339
  Sequence 30, Application US/08713557B Patent No. 5912168
  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
  APPLICANT: Moore, K. APPLICANT: Nagle, D.
  GENERAL INFORMATION:
   SOFTWARE: FastSEQ for Windows Version 3.0
  LENGTH: 90050
TYPE: DNA
ORGANISM: Mus musculus
   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,557B
FILING DATE: 30-AUG-1996
   APPLICANT: Watson, James APPLICANT: Rudert, Fritz
   2968 AGACTGCCAAAGAGCTATC 2950
  FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  COMPUTER READABLE FORM:
  CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION:
   NUMBER OF SEQUENCES:
   ATTORNEY/AGENT INFORMATION:
                       NAME: Speckman, Ann W REGISTRATION NUMBER:
  FILING DATE:
  MEDIUM TYPE:
   COUNTRY:
   STATE:
   CITY: Seattle
  STREET:
   1 aaactacctaagagctatc 19
| ||| || ||||||||||
     REFERENCE/DOCKET NUMBER:
  ADDRESSEE:
  1 aaactacctaagagctatc 19
   98121
   WΑ
  E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
   USA
   Conservative
  Diskette
   AND TRANSCRIPTION FACTORS: 38
   71.0%;
   CD95 REGULATORY GENE SEQUENCES
  James D.
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  US-08-322-742-9
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  Sequence 9, Applicatic Patent No. 5688641 GENERAL INFORMATION:
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  Query Match
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  PILING DATE:
PATOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
APPLICATION NUMBER: 1991
  TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
   NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
  INFORMATION FOR SEQ ID NO:
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
  SEQUENCE CHARACTERISTICS:
  APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
  SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
   TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
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  STRANDEDNESS:
  TOPOLOGY:
   LENGTH:
   APPLICATION NUMBER:
   COUNTRY:
  CITY: Boston
STATE: Massa
  ADDRESSEE: F15H ...-
cmrref: 225 Franklin Street
  TOPOLOGY: 11
  Local Similarity
   l aaactacctaagag 14
  14; Conservative
   RY: U.S.A.
02110-2804
   nucleic acid
  Massachusetts
   Application US/08322742
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                 Score 13.8;
Pred. No. 97;
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Gaps
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US-08-998-416-670
  US-08-998-416-670
Sequence 1, Application US/09073587
Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: Li, Yi
   Matches
   Query Match
  Sequence 670, Application US/08998416 Patent No. 6239264
   TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
   GENERAL
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
   SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
  TELECOMMUNICATION INFORMATION:
  168 AAAATACCAAAGAGCTA 184
  CORRESPONDENCE ADDRESS
  APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
  APPLICANT:
APPLICANT:
   APPLICANT:
   Local Similarity
   TELEPHONE: 919-541-8689
  ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
   TOPOLOGY:
  1 aaactacctaagagcta 17
  STRANDEDNESS:
   FILING DATE:
   APPLICATION NUMBER:
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  1 aaactacctaagagcta 17
   INFORMATION:
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  Wendland, Jurgen
Knechtle, Philipp
  Mohr, Christine
   Pohlmann, Rainer
Steiner, Sabine
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  linear
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N: 435
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NUMBER OF INVENTION: Transgenic Seedless Plants
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORREST: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STREE: 5170 Manhattan Circle, Suite 201
CITY: Boulder
STREE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYRE: PLOPY disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM PC compatible
OPERATION UNMER: US/09/073,587
FILING DATE: 06-MAY-1998
CILASTFICATION COUNTRY US/09/073,587
FILING DATE: 06-MAY-1998
CILASTFICATION
COMPTER: 06-MAY-1998
CILASTFICATION
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Gaps

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| •<br>· |   |   |
| i.     |   | • |
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No.
  Minimum DB
Maximum DB
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   OM nucleic - nucleic search, using sw model
  Database
  Post-processing:
   Total number of hits satisfying chosen parameters:
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  on:
   987654321
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Maximum Match 100%
Listing first 45 summaries
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ABL11013
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ABL34419
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  ; Search time 1139.19 Seconds (without alignments) 30.143 Million cell updates/s
  Human CD95 recepto
Fas promoter regio
Drosophila melanog
Drosophila melanog
   Description
                Human immune syste
Drosophila melanog
Phosphatidyl inosi
   cell updates/sec
 Drosophila
   Drosophila melanog
 melanog
   ဂ ဂ
  o o
  a
   000000
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0000000

| Human reproductive | AAL03699 | 22 | 12304 | 76.0 |      | 45         |
|--------------------|----------|----|-------|------|------|------------|
| Human ovarian and  | ABA07882 | 22 | 12304 | 6    | 15.2 | 44         |
|                    | ABL32096 | 24 | 6357  | σ.   |      | 43         |
| O                  | ABL34003 | 24 | 6204  | 76.0 |      | 42         |
| н                  | AAS45482 | 22 | 6204  |      |      |            |
| metas              | ABL34564 | 24 | 6012  | 6.   |      |            |
| Human immune syste | ABL32085 | 24 | 5945  |      |      | 39         |
| Human regulation f | AAA98383 | 21 | 3262  | σ.   |      | 38         |
| -length            | AAK94738 | 22 | 2922  |      |      | 37 ·       |
|                    | ABL25058 | 23 | 2918  | 6.   |      | 36         |
| Drosophila melanog | ABL19508 | 23 | 2447  | σ.   |      | 35<br>5    |
| O                  | ABA14997 | 22 | 2328  | S.   |      | 34         |
| Drosophila melanog | ABL27108 | 23 | 2276  | S.   |      | ယ          |
| Drosophila melanog | ABL06426 | 23 | 1865  | S.   |      | 32         |
| Zea mays DNA fragm | AAC43644 | 21 | 1061  | σ    |      | 31         |
| Probe #2092 used t | AAI02101 | 22 | 498   | σ    |      | 30         |
|                    | AAI33534 | 22 | 498   | σ    |      | 29         |
| Probe #2121 for ge | AAI12188 | 22 | 498   | 76.0 |      | 28         |
|                    | AAK02157 | 22 | 498   | g    | •    | 27         |
| Probe #2106 for ge | ABA23640 | 22 | 498   | σ,   |      | 26         |
| al                 | ABA53892 | 22 | 498   | ა    | •    | 25         |
| æ                  | ABL19509 | 23 | 447   | ა    |      | 24         |
|                    | ABL27109 | 23 | 276   | ა    |      | 23         |
|                    | AAX06819 | 20 | 2526  | 77.0 | 15.4 | 22         |
| Genomic fragment # | AAF28547 | 22 | 89047 | 9    | 15.8 | 21         |
| Human breast cance | AAL26789 |    | 6788  | 9.   | •    | 20         |
| Human immune/haema | AAK80489 |    | 4663  | 9    | •    | 19         |
| DNA encoding novel | AAS86514 |    | 3293  | 9    | •    | 18         |
| Human full-length  | AAK94811 |    | 2864  | .9   | 5    | 17         |
| Human zrnpl (ribon | AAA09173 | N  | 2755  | ۰    | 15.8 | 16         |
| Human type II GnRH | AAV21213 | ш  | 1642  | .o   | 5    | 15         |
| Human breast cance | AAF17582 | N  | 1022  | ٥    |      | 14         |
| Human breast cance | AAS47012 | N  | 1022  | .0   |      | <u>1</u> 3 |
| Drosophila melanog | 030      | 23 | 17358 |      |      | 12         |
|                    | 유        |    | 17344 | 84.0 | 16.8 | 11         |
| Drosophila melanog | ABL20119 |    | 7191  | 84.0 | 16.8 | 10         |

## ALIGNMENTS

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  Human CD95 receptor promoter DNA p53 binding fragment #3.
  Krammer P, Mueller-Schilling M, Oren
   16-OCT-1998;
   16-OCT-1998;
  03-FEB-2000.
   DE19847779-C1.
  Homo sapiens.
   11-MAY-2000
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  2000-162245/15
   (first entry)
   98DE-1047779
   98DE-1047779
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Novel receptor DNA useful for substances potentially useful

identifying apoptosis-modulating
for cancer chemotherapy -

```
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  protein_bind
   protein_bind
  protein_bind
  protein_bind
  protein_bind
  protein_bind
   protein_bind
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   Key
  Homo sapiens
  Fas promoter region
  22-OCT-1996
   AAT34162;
   AAT34162 standard; DNA; 1608
  This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor promoter which is capable of
  Sequence 20 BP; 8 A; 5 C; 2 G;
   Claim
  gene promoter; apoptosis; ageing; autoimmune disease;
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  DB 21;
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  binding
  binding
  binding site
  binding site
   20;
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   site
   0
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   0;
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XX
  밁
   RESULT
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Best Local
   Matches
  defined as the Fas gene promoter region. This includes a number of transcription factor binding sites. A coding sequence for the N-terminal portion (AAR99471) of the Fas protein leader peptide is also included. The DNA segment was isolated from a human placental DNA library using a 32P-labeled segment of human Fas cDNA corresponding to nt 23-346. It can be combined with a structural gene so that the gene is under the transcriptional control of the transcription factor binding sites. The promoter region can be used to regulate Fas gene expression, e.g. in tumour or immune cells, as a means of treating Fas-mediated apoptosis disorders such as
                          27-SEP-2001.
23-MAR-2001; 2001WO-US09231.
   WO200171042-A2
   Drosophila melanogaster.
   pharmaceutical;
  Drosophila;
  Drosophila melanogaster expressed polynucleotide SEQ ID NO 27521
   26-MAR-2002
  ABL11013;
   ABL11013 standard;
   Sequence 1608 BP;
  malignancies and autoimmune diseases.
  A novel DNA segment (AAT34162) has an isolated sequence region defined as the Fas gene promoter region. This includes a numb
  Claim 11; Fig 2; 123pp; English.
  Human Fas gene promoter region - used : expression and for developing products apoptosis disorders
  P-PSDB; AAR99471.
  WPI; 1996-354527/35.
  (UABR-) UAB RES FOUND
   20-JAN-1995;
  507 aaactacctaagagctatct 526
   19-JAN-1996;
   25-JUL-1996.
   W09622370-A1
  intron
  Local Similarity
   1 aaactacctaagagctatct
   ω
  Koopman WJ,
   developmental biology; cell signalling; insecticide;
  Conservative
   (first entry)
  95US-0377522
   gene;
   96WO-US00606
   /codon_start=1479..1469
/product= Fas protein leader
1497..1608
   /note=
   /*tag=
  398 A; 421 C; 423 G; 366 T; 0 other;
   cDNA; 1737
   100.0%;
  88
  Liu
  "5' end of intron 1 (full length approx 14 kb"
   ú
   0,
   Score 20;
Pred. No.
   Mountz JD,
  Mismatches
  for heterologous protein for treating Fas-mediated
   0.55;
   Zhou
  17;
   0,
   Ή;
  Length 1608;
   0,
   Gaps
```

```
RESULT 4
ABL09420/c
   Š
  Query Match
Best Local
  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL97277-ABR72072)
   23-MAR-2000;
11-JUL-2000;
   1576 aaactacccaagagctatc 1594
  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
  The invention relates to an isolated nucleic acid detection reagent
  Claim 1; SEQ ID NO 27521; 21pp + Sequence Listing; English
   genes from Drosophila and
   New isolated nucleic acid
  Venter JC,
   (PEKE ) PE CORP NY.
New isolated nucleic acid
                       WPI; 2001-656860/75
P-PSDB; ABB65317.
  23-MAR-2000;
11-JUL-2000;
   23-MAR-2001; 2001WO-US09231
  27-SEP-2001
  WO200171042-A2
  Drosophila melanogaster
  pharmaceutical; gene; ss.
  Drosophila; developmental biology;
   Drosophila melanogaster expressed polynucleotide
   26-MAR-2002
  ABL09420;
   ABL09420 standard;
  Sequence 1737 BP;
   Venter JC,
   (PEKE ) PE CORP NY.
   ABB57737-ABB72072)
   L
   aaactacctaagagctatc 19
   2001-656860/75.
  Similarity
  ABB66910
  Adams M,
   Adams M,
   Conservative
   2000US-191637P.
2000US-0614150.
  2000US-191637P.
2000US-0614150.
  (first entry)
   446 A; 460 C;
  cDNA; 2815
  87.0%;
94.7%;
  Ľi
   Ŀ
  PWD,
   detection reagent for detecting for elucidating cell signalling
detection reagent for detecting 1000
   0,
  Score 17.4;
Pred. No. 13;
  Myers
   Myers
  Mismatches
   475 G;
   cell
  ₩;
  356 T; 0 other;
   signalling; insecticide;
  DB
   23;
   <u>,</u>
   SEQ
  Indels
   Length
   IJ
   Ö
   1737;
  and
   1000 or more
   0;
   cell-cell
 or
  Gaps
  more
   WIPO
  ST
  0;
```

```
밁
  QΥ
   Query Match
Best Local S
  Matches
   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
   The sequence data for this patent did not form part of the prispecification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
  genes from Drosophila and for elucidating cell signalling and interactions \boldsymbol{\cdot}
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
   Drosophila melanogaster expressed polynucleotide SEQ ID NO 27518
   ABL11012 standard; cDNA; 3916
  2076 AAACTACCCAAGAGCTATC 2058
  Sequence 2815 BP; 653 A; 671 C; 708 G; 783 T; 0 other;
  The invention relates to an isolated nucleic acid detection reagent
   Claim 1; SEQ ID NO
  genes from Drosophila
   New isolated nucleic
   Venter JC, Adams M,
   23-MAR-2000;
11-JUL-2000;
  23-MAR-2001;
   27-SEP-2001.
  WO200171042-A2
  Drosophila melanogaster.
  pharmaceutical;
  Drosophila;
   26-MAR-2002
   ABL11012;
  interactions -
   (PEKE ) PE CORP NY
   1 aaactacctaagagctatc 19
|||||||| ||| |||||||
  2001-656860/75.
  l Similarity
18; Conserv
  ABB66909.
   SEQ ID NO 22742; 21pp + Sequence Listing; English
  developmental biology; cell signalling; insecticide;
  Conservative
  2000US-191637P
2000US-0614150
  2001WO-US09231
  (first entry)
   gene;
   27518; 21pp + Sequence Listing; English.
   87.0%;
94.7%;
  acid
a and
   Ŀ
   PWD,
  detection reagent for detecting 1000 for elucidating cell signalling and c
  0.
  Score
Pred.
   Myers
   Mismatches
  17.4;
No. 1;
  띨.
   BB
   23;
  1;
   Indels
   Length
   2815;
  printed
   0;
   0 or more
cell-cell
  cell-cell
   Gaps
  WIPO
   is
   ST
```

0,

```
RESULT 6
ABL34419/c
ID ABL3444
XX ABL344
XX ABL344
XX ABL344
XX Human;
XX Human;
XX Human;
XX Human;
XX Human;
XX Homo s
YX Homo s
XX Homo s
YX Homo s
XX Homo s
YX Ho
   밁
   ភភភភ×្ល
  Query Match
Best Local Similarity
   Matches
   Query Match
   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid_arthritis, psoriasis and inflammatory/ulcerative bowel
  Sequence 1608
  Claim 1; SEQ ID NO 2392;
  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
   cytosine methylation
  Nucleic acid comprising frag
   WPI; 2002-130909/17.
  30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826
  (EPIG-)
  02-JUL-2001; 2001WO-EP07537.
  03-JAN-2002.
  WO200200928-A2
   1162 AAACTACCCAAGAGCTATC
  Homo sapiens.
   Human immune system associated gene SEQ ID NO: 2392.
  26-MAR-2002 (first entry)
   ABL34419 standard;
   Sequence 3916 BP; 1026 A; 965 C; 927 G; 998 T;
  ABL34419;
  (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
   Local Similarity 94.7
mes 18; Conservative
   1 aaactacctaagagctatc 19
   EPIGENOMICS AG.
  Piepenbrock C,
  The present sequence is a gene of the
  BP;
   366 A;
  DNA;
     90.0%;
  87.0%;
94.7%;
  fragment of chemically modified went of diseases associated with
  51
   32pp + Sequence Listing; German.
  1608 BP
  Berlin
   1144
   Ç
Score
Pred.
   0,
  Pred.
  Score 17.4;
   421
  <u>~</u>
   Mismatches
16.8;
No. 27;
   ç,
  No.
   770
  14;
                        DВ
  T; 0 other;
  DB
  23;
  <u>ب</u>
  invention.
   0 other;
                     Length 1608;
  Indels
  Length
   directly from
   gene, useful
abnormal
  3916;
   0;
   Gaps
   WIPO
   0;
```

```
XXXX
                                   IJ
   Db
   AAT80200
  В
   Qy
   ABL18046
   Matches
  Query Match
   Matches
          AAT80200
   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                 AAT80200 standard;
   Sequence 2279 BP;
  at ftp.wipo.int/pub/published_pct_sequences.
  The sequence data for this patent did not form specification, but was obtained in electronic f
   Claim 1; SEQ ID NO 5611; 21pp + Sequence Listing; English.
   New isolated nucleic acid
genes from Drosophila and
   WPI; 2001-656860/75.
  23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
   1102
  622 aaactacctaagacgtatct 641
  (PEKE ) PE
   23-MAR-2001; 2001WO-US09231
  Drosophila; dev pharmaceutical;
  ABB57737-ABB72072)
   Venter JC,
   WO200171042-A2
   Drosophila melanogaster.
   Drosophila melanogaster genomic polynucleotide SEQ ID NO 5611.
  ABL18046;
  ABL18046 standard; DNA; 2279
  26-MAR-2002
   Local Similarity
nes 18; Conser
   1 aaactacctaagagctatct 20
  8
   Н
   7
  AAACTACCTAAAAACTATCT 1083
  aaactacctaagagctatct 20
   18;
  CORP NY.
   Adams M,
  Conservative
   developmental biology; cell signalling; insecticide;
  Conservative
  (first entry)
  gene;
   751 A; 417 C; 442 G; 669
                                 cDNA; 6831 BP
   84.0%;
90.0%;
   Li PWD,
  this patent did not form part of the printed obtained in electronic format directly from WIPO
  detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
   0;
  Score 16.8;
   Pred.
   0,
  ВP
  Myers EW;
   Mismatches
   Mismatches
  No.
  28;
  DB
   Ŧ,
   0 other;
  2
  2
  Indels
  Length
  Indels
   2279;
  and cell-cell
  0;
  0;
  Gaps
   Gaps
  ı.
   0;
```

22-JUN-1998

(first entry)

```
ABL10307
ID ABL1
XX
AC ABL1
XX
  밁
   RESULT
   This cDNA sequence codes for cpk (see AAW38757), a Drosophila polypeptide that belongs to a novel class of phosphatidyl inositol 3-kinases that contain a C2 domain, are capable of phosphorylating a D3 hydroxyl of an inositol ring in phosphatidyl inositol and capable of property inositol and phosphatidyl inositol and phosphatidyl inositol and phosphatidyl inositol and capable of protein sorting. Short fragments of cpk cDNA were obtained from a sorting. Short fragments of cpk cDNA were obtained from a companie were used to screen the CDNA library to obtain larger fragments, and missing 5' ends were obtained by RACE. A recombinant host cell, transfected with a vector comprising a cpk nucleic acid is claimed. Novel phosphatidyl inositol 3-kinases can be used to screen for agonists/antagonists of activity and in a claimed method of treating a disorder caused by dysregulation of a growth factor activation signalling cascade. Antagonists
  Query Match
  Matches
  Phosphatidyl inositol 3-kinase; signal transduction; cell cycle; antagonist; inflammatory joint disease; cell proliferation; cancer; psoriasis; restenosis; atherosclerosis; therapy; diagnosis; cpk; ss.
   Key
  New isolated phospatidyl inositol-3 kinase polypeptide - used to develop products for diagnosis and therapy, particularly for proliferative disorders, e.g. inflammatory joint diseases, or cancer
   WPI; 1997-448442/41.
   Chen Y,
   29-FEB-1996;
   04-SEP-1997.
  WO9731650-A1
  Drosophila melanogaster
   may reduce Ras activation allowing treatment of proliferative disorders such as atherosclerosis, inflammatory joint disease, psoriasis, restenosis following angioplasty, and cancer.
   (REGC ) UNIV CALIFORNIA.
   12-FEB-1997;
            ABL10307;
                                    ABL10307 standard;
  6690
  Sequence 6831 BP; 1829 A; 1685 C; 1669 G; 1648 T; 0 other;
   Example 1; Fig 9; 77pp; English.
  Local Similarity
  1 aaactacctaagagctatct 20
   9
   amactacctaagacgtatct 6709
   AAW38757.
  Molz L, Williams LT;
   inositol 3-kinase cdk cDNA
  Conservative
  96US-0609049
   97WO-US02193
   Location/Qualifiers
148..5778
/*tag= a
                                    cDNA; 6871 BP
  84.0%;
  Score 16.8;
Pred. No. 3
  Mismatches
   DB 18; | Length 6831;
  2
  Indels
   0;
   0,
   RESULT 1
ABL20119
  γ
```

```
Query Match
Best Local Similarity
   Matches
  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
  New isolated nucleic acid genes from Drosophila and interactions -
   WO200171042-A2
  Drosophila melanogaster.
  pharmaceutical;
   Drosophila; developmental biology; cell signalling; insecticide;
   Drosophila melanogaster expressed polynucleotide SEQ ID NO 25403
   Sequence 6871 BP; 1830 A; 1690 C; 1669 G; 1682 T; 0 other;
  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
   The invention relates to an isolated nucleic acid detection reagent
   Claim 1; SEQ ID NO 25403; 21pp + Sequence Listing; English.
   WPI; 2001-656860/75.
   Venter JC,
  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
  23-MAR-2001; 2001WO-US09231
  27-SEP-2001.
  26-MAR-2002
   pharmaceutical; gene;
  Drosophila; developmental biology; cell signalling; insecticide
   Drosophila melanogaster genomic polynucleotide SEQ ID NO 11830.
  26-MAR-2002
  ABL20119;
   ABL20119 standard; DNA; 7191 BP
  6731 aaactacctaagacgtatct 6750
   at ftp.wipo.int/pub/published_pct_sequences.
   P-PSDB; ABB66204.
  (PEKE ) PE CORP NY
Drosophila melanogaster
   (ABB57737-ABB72072
   1 aaactacctaagagctatct 20
   10
   18;
   Adams M,
  Conservative
  (first entry)
   (first entry)
  gene;
  84.0%;
90.0%;
   Ŀi
   PWD,
   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
  0;
  Score 16.8;
Pred. No. 31;
   Myers EW;
  Mismatches
  DВ
   23;
  2;
  Length 6871;
  0;
  from
   cell-cell
  Gaps
  WIPO
  Ľ
  0;
```

WO200171042-A2

```
밁
  Š
   RESULT 11
  Query Match
Best Local
  Matches
       New isolated nucleic
                             WPI; 2001-656860/75.
  Venter JC,
   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
  WO200171042-A2
   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins sequences (ABL01840-ABL16175) and the encoded proteins
  23-MAR-2001; 2001WO-US09231.
  Drosophila
  pharmaceutical;
   Drosophila; developmental
  Drosophila melanogaster genomic polynucleotide SEQ
   (PEKE ) PE CORP NY.
  26-MAR-2002
   ABL20118;
  ABL20118 standard; DNA; 17344
  7051 aaactacctaagacgtatct 7070
  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
  Sequence 7191 BP; 1931 A; 1730 C; 1740
   Claim 1; SEQ ID NO 11830; 21pp + Sequence Listing; English
  genes from Drosophila and
  New isolated nucleic acid
   (PEKE ) PE CORP NY
  23-MAR-2000;
11-JUL-2000;
  23-MAR-2001;
  interactions
  1 aaactacctaagagctatct 20
   ftp.wipo.int/pub/published_pct_sequences.
   2001-656860/75
  Similarity
  melanogaster
  Adams M,
   Conservative
   Adams M,
   (first entry)
   2000US-191637P
2000US-0614150
  2001WO-US09231
  gene;
       acid
  84.0%;
90.0%;
   Li PWD,
  PWD,
     detection
   biology; cell signalling;
   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
  Score 16.8;
Pred. No. 3;
   ВP
   Myers
   Myers
  Mismatches
     reagent
   EW;
   31,
  ç;
  DB
  1790 T;
     for
  23;
  2
   detecting 1000 or
  0
   Indels
   Length
  ID NO 11827.
  insecticide;
  other
  7191;
   The invention
  0,
   from
   cell-cell
  Gaps
    more
  WIPO
  and
  LS
  0
```

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밁
  RESULT 12
ABL10306
   Ωy
  Matches
   Query Match
Best Local
   16204 aaactacctaagacgtatct 16223
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
  Claim 1; SEQ ID NO 25400;
   New isolated nucleic
   P-PSDB; ABB66203
   Venter JC,
  (PEKE ) PE CORP NY.
  23-MAR-2000;
  23-MAR-2001; 2001WO-US09231
   27-SEP-2001.
  Drosophila melanogaster
   pharmaceutical;
  Drosophila; developmental
  Drosophila melanogaster expressed polynucleotide SEQ ID NO 25400
  ABL10306 standard; cDNA; 17358 BP
  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
  Interactions
  11-JUL-2000;
  26-MAR-2002
   ABL10306;
   Sequence 17344 BP; 4659 A; 3886 C;
  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
   Claim 1; SEQ ID NO 11827; 21pp + Sequence Listing; English.
   genes from Drosophila and for elucidating cell signalling and
   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
  interactions
   1 aaactacctaagagctatct 20
  ftp.wipo.int/pub/published_pct_sequences.
  2001-656860/75
   solated nucleic acid
from Drosophila and
   18;
  Similarity
   Adams M,
   Conservative
  2000US-191637P
2000US-0614150
   (first entry)
   gene; ss.
  84.0%;
   Ŀi
   PWD,
  21pp + Sequence Listing; English
   detection reagent for detecting for elucidating cell signalling
   biology;
  Score 16.8;
Pred. No. 34
   Myers
  Mismatches
   cell signalling;
   3857 G; 4942 T; 0 other;
   ¥
   DB
   23;
  2;
   Length 17344;
  Indels
  . The invention i
   0;
  cell-cell
   cell-cell
  or more
   Gaps
   WIPO
   is
  is
   0;
```

```
RASSULT 1
AAS470125
ID AAS470125
ID AAS470125
AX AAS4
AX BAAS4
AX AAS4
AX BAAS4
AX BAASA
AX B
   밁
  SSSSXX
The invention relates to isolated breast tumour proteins and conclude acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the corrections. Also included are expression vectors expressing the proteins and substitute the proteins or concluded and antibodies raised against the proteins and can antigen presenting cell expressing the protein. The proteins and concluded with inappropriate breast tumour protein expression, concluded with inappropriate breast tumour protein expression, concluded with inappropriate breast tumour protein expression, concluded and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic casanys to detect and quantitrate the presence of similar nucleic acids in concludes, and therefore which patients may be in need of restorative concludentify modulators (e.g. antagonists) of breast tumour protein concludes and antibodies may also be used to down regulate expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used constant and the proteins in the presence of the proteins in the presence of the proteins in the presence of the proteins in the constant assay (ELISA)) and in other constant and present tumour cDNA library isolated by subtractive
  Query Match
Best Local
  Matches
   16218
   WPI;
   Jiang
  Claim 1; Page 165; 297pp; English.
  diagnosis
  Breast
   17-APR-2000; 2000US-0551621.
08-JUN-2000; 2000US-0590751.
22-JUN-2000; 2000US-0604287.
20-JUL-2000; 2000US-0620405.
   gene
  Human;
  Human breast cancer cDNA clone B725P
   AAS47012 standard; cDNA; 1022 BP
   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
   (CORI-) CORIXA CORP.
  12-APR-2001; 2001WO-US12164
  25-OCT-2001.
   W0200179286-A2
   Homo sapiens
   18-DEC-2001
   AAS47012;
   Sequence 17358 BP; 4664 A; 3890 C;
  (ABB57737-ABB72072).
   13
   1 aaactacctaagagctatct 20
  ftp.wipo.int/pub/published_pct_sequences.
   2001-611721/70.
  therapy.
   aaactacctaagacgtatct 16237
  Υ,
  SS;
  Similarity
   Dillon DC,
  mour Proteins and nucleic acids useful and treatment of breast cancer -
   breast
   Conservative
   (first entry)
   cancer protein; tumour; cancer;
  84.0%;
90.0%;
   Mitcham
  0
  Score 16.8;
Pred. No. 34;
   JĽ,
   Mismatches
   3861 G;
  Xu J,
   Harlocker SL,
  DВ
   4943 T; 0 other;
  23;
   2;
   for the
  cytostatic;
   Indels
   Length 17358,
  prevention,
   Hepler WT
   0;
   Gaps
  WIPO
   0;
```

RESULT 1
AAV21213
ID AAV2
XX
AC AAV2

15

AAV21213 standard; DNA; 1642 BP

AAV21213;

```
RESULT 1
AAF17582
밁
  밁
  δÃ
  Soxco
                Š
                                   Matches
  Query Match
Best Local
  Matches
  Query Match
  02-APR-1999;
23-JUN-1999;
02-SEP-1999;
03-NOV-1999;
  The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
   a breast tumor protein
  Sequence 1022
   particularly breast tumours.
   Claim 6; Page 105-106;
  An isolated polypeptide useful for the tumors e.g. breast cancer comprises at
   WPI;
   Yuqiu J,
   15-FEB-2000; 2000WO-US05308
  12-0CT-2000
  WO200060076-A2
   Homo
  Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss
  Human breast
  13-MAR-2001
  AAF17582;
   AAF17582 standard; cDNA; 1022
   Sequence 1022 BP; 254 A;
  hybridisation against a normal breast cDNA library.
  (CORI-) CORIXA CORP.
539
   539
  Local
   14
                 N
   2 aactacctaagagctatct 20
acctacctaatagctatct
        aactacctaagagctatct 20
   2001-122627/13.
  acctacctaatagctatct
  sapiens
                                   l Similarity
17; Conser
   17; Conservative
   Dillon DC,
                                   Conservative
   cancer
  BP;
  (first
   99US-0339338
99US-0389681
   99US-0433826
  99US-0285480
  254
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23-JUL-1998 (first entry)

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Search completed: September 7, 2002, 18:40:29 Job time: 29923 sec
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Matches 17; Conservative
   This sequence encodes a novel human type II gonadotropin-releasing hormone receptor (GnRHR II) polypeptide. This protein and its products can be used for identifying compounds which modulate GnRHR II-mediated metabolism in cells. Compounds identified as agonists or antagonists can be used for treating hormone-dependent tumours. Agonists and antagonists may also prove useful in the study of GnRHR II-directed neuromodulation of sexual behaviour, e.g. agonists may be used in the treatment of diminished libido and impotence. The products can also be
   New isolated type II gonadotropin-releasing hormone receptor - used to develop products for use in the treatment of hormone-dependent tumours or for neuromodulation of sexual behaviour
   Type II Gonadotropin releasing hormone receptor; GnRH-H II; impotence; identification; diagnosis; detection; modulator; treatment; libido; hormone-dependent tumour; neuromodulation; sexual behaviour; ds.
  Sequence 1642 BP; 449 A; 399 C; 324 G; 470 T; 0 other;
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   Claim 11; Page 37-38; 54pp; English.
   WPI; 1998-168750/15.
  Conklin DC,
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  13-JUN-1996;
   11-JUN-1997;
  18-DEC-1997
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1 (bases 1 to 20)

Mueller-Schilling, M., Krammer, P. and Oren, M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 16 03-FEB-2000;

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1 (bases 1 to 40)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 19847779-C 30 03-FEB-2000;

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1 (Dases 1 to 40)

Mueller-Schilling, M., Krammer, P. and Oren, M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 22 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
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Krammer, P.H.
Direct Submi
  Behrmann, I., Walczak, H. and Krammer, P.H. Structure of the human APO-1 gene
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J. Immunol. 154 (3), 1239-1245 (1995)
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Cheng, J., Liu, C., Ko
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   Characterization of human Fas gene.
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   820 AAACTACCTAAGAGCTATCT 839
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   Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Tel:076-234-4424, Fax:076-234-4480)
  Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection J. Biol. Chem. 270 (30), 18007-18012 (1995)
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2165)
   Homo sapiens
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  D31968.1
   D31968
  Human DNA for Fas antigen, promoter
  2 (bases 1 to 2165)
Nakanishi,Y.
  Wada, N., Matsumura, M., Ohba, Y., Kobayashi, N., Takizawa, T.
  Homo sapiens blood DNA, clone pF7.
   Direct Submission
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Conservative (
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AAACTACCTAAGAGCTATCT 1403
   Submitted (26-MAY-1995) F.H. Rudert, Genesis Research Development, Corporation Ltd., PO Box 50, Auckland, NE Overlaps with X81335, & x82279-X82286.

Location/Qualifiers
   H.sapiens CD95 gene 5' flanking region.
   Similarity
  Direct Submission
   Rudert, F.H
   96069539
   DNA Cell Biol. 14 (11),
  Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2344)
  Similarity 100.0%;
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  Identification of a silencer, enhancer, and basal promoter region in the human CD95 (Fas/APO-1) gene
   Watson,J
  Homo sapiens
  beta interferon; CD95 gene; silencer.
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1 (bases 1 to 2827)
Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 4 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
Location/Qualifiers
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Sequence 4 from Patent DE19847779.
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   Novel receptor dna useful for identifying apoptosis modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 3 03-FEB-2000;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2380) Mueller-Schilling,M., Krammer,P. and Oren,M.
   2380 bp
Sequence 3 from Patent DE19847779.
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  Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847/79-C 1 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
   corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, was compared to the MCRNDEP of t
  AX026089.1 GI:10187520
  on Aug 31, 2001 this sequence version replaced gi:14161146. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
  1 (bases 1 to 3212)
Mueller-Schilling, M., Krammer, P. and Oren, M.
                                     http://www.sanger.ac.uk/HGP/Chr10
RP11-399019 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10 constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at
  Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
   Blakey,S.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
  Homo sapiens
  complete sequence. AL157394
   Human DNA sequence from clone
   AL157394
  Mammalia;
   Eukaryota;
   Homo sapiens
  SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
   requests: clonerequest@sanger.ac.uk
  Direct Submission
  AL157394.15 GI:15384622
http://www.chori.org/bacpac/home.htm
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Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Davy-Carroll, L., Declerich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulse, R., Martinez, B., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Martinez, B., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Morgan, M., Morris, S., Moser, M., Nickerson, E., Nwokenkwo, S., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
  Muzny,D.M., Adams,C., Addo-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J. Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Benton,J., Bineye,K., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Chacko,J., Chavez,D., Chen,G., Chen,R., Carazos,S.R., Chacko,J., Chavez,D., Chen,G., Cox,C., Chen,Z., Chowdhry,I., Christoppulos,C., Cleveland,C.D., Cox,C., Chen,Z., Chacker, C., Chen,G., Chen,C., Ch
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   Rattus
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  Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tangy, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
  Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
   findPhrapList
  Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Scott, G., Shen, H., Shooshtari, N., eigen, T. Control Foreit Control Fo
  2 (bases 1 to 172269)
Worley, K.C.
  Direct Submission
   Unpublished
   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
  runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
   as soon as it is available and the accession number will be preserved.
  Consensus quality: 145908 bases at least Q40 Consensus quality: 152564 bases at least Q30 Consensus quality: 158487 bases at least Q30 Estimated insert size: 150457; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.7x in Q20 bases; sum-of-contigs estimation
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of 1782
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   Submitted (20-AUG-2001) Whitehead Instituté/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
   Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
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  Unpublished
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  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
  NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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9345 9444: gap of
9445 13083: contig of 3639 bp in length
13084 13183: gap of
13084 13183: gap of
13084 13183: gap of
13084 1545: contig of 2562 bp in length
15746 15845: gap of
15846 20539: contig of 4694 bp in length
20540 20639: gap of
20640 62896: contig of 42257 bp in length
20640 62896: contig of 42257 bp in length
   as soon as it is available and the accession number will
  Insert size: 250000; agarose-fp
Insert size: 245397; sum-of-contigs
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
  Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.96x1 Consensus quality: 242847 bases at least Q40 Consensus quality: 244315 bases at least Q30 Consensus quality: 244906 bases at least Q20
   Center project Information Center project name: L14296 Center clone name: 57_F 18
  Contact: sequence_submissions@genome.wi.mit.edu
  Sequencing vector: Plasmid; n/a;
   193685 193784: gap of 100 bp
193785 245997: contig of 52213 1
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (base 1 to 1814)
1 (base 1 to 1814)
   sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web Site (http://fruitfly.berkeley.edu) or send email to
  Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
  Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Chawez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
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Drosophila melanogaster
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Location/Qualifiers
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481
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   JOURNAL
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2 (bases 1 to 154771)

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Karra, K., Kearney, L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lewis, S., Li, P., Lomotan, M. A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
  This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
  Submitted (06-AUG-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Sep 6, 2001 this sequence version replaced gi:13324753. Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
   Drosophila melanogaster, chromosome 2L, region 33E-33F, BAC clone BACROSED9, complete sequence.
   Direct Submission
   Rubin, G.M.
   Unpublished
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   Berkeley, CA 94720
   fruit fly.
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Indels 0; Gaps

0;

Search completed: September 7, 2002, 18:23:58 Job time: 28937 sec

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Copyright (c) 1993 - 2000 Comp
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| 40                                                                                                                                                                                                                                                                                                                                                           | US: S GP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      | 000 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
| est 1<br>200<br>200<br>212<br>213<br>213                                                                                                                                                                                                                                                                                                                     | SOLUTION OF 290                                                |      | 222<br>222<br>232<br>232<br>232<br>233<br>244<br>244<br>244<br>244                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |  |
| O                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |      | 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |  |
| larity Consey tyacac         tyacac         ggctgg ggctgg               ccaggc                                                                                                                                                                                                                                                                               | plicati<br>4055<br>arion:<br>an, nicuson<br>rcusson<br>NTION:<br>E: ISPH<br>CATION<br>G DATE:<br>ID NOS<br>entin v<br>entin v<br>entin v<br>entin v<br>entin v<br>21)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10)(1<br>10). |      | 777777777777777777777777777777777777777                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
| vative                                                                                                                                                                                                                                                                                                                                                       | on US/0 holas w Eric Antisen O351 NUMBER 1999-C : 85 Cer. 2.C er. 2.C er. 2.R hem. hem.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |      | 421<br>421<br>421<br>421<br>421<br>421<br>421<br>585<br>585<br>585<br>1679<br>1679<br>1679<br>1679<br>1679<br>12141<br>12141<br>12141<br>12141<br>12141<br>1314<br>444<br>444<br>444<br>444<br>444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |  |
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| 10; p                                                                                                                                                                                                                                                                                                                                                        | Com<br>19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      | US                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |  |
| MISmar<br>MISmar<br>agacgcti<br>agacgcti<br>gggcactt<br>      <br> -    <br>gggcactt<br>gggcactt<br> -     <br> -                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ≥    | 0.08-48 0.08-48 0.08-48 0.08-28 0.08-33 0.08-38 0.08-38 0.08-38 0.08-38 0.08-38 0.08-38                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
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| )066<br>1126<br>120<br>1186<br>186<br>80<br>80                                                                                                                                                                                                                                                                                                               | <b>–</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      | 24. Appl<br>24. Appl<br>24. Appl<br>24. Appl<br>24. Appl<br>27. Appl<br>27. Appl<br>11. Appl<br>10. Appl<br>10. Appl<br>11. Appl<br>11. Appl<br>11. Appl<br>11. Appl<br>12. Appl<br>13. Appl<br>14. Appl<br>15. Appl<br>16. Appl<br>17. Appl<br>18. Appl<br>19. Appl<br>19. Appl<br>19. Appl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |  |
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  RESULT 2
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  Query Match
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  Sequence 18, Application US/08444231 Patent No. 5652210
  TELEX: 706141
INFORMATION FOR SEQ ID NO:
   GENERAL INFORMATION:
2153 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg
   2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
  REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415),813-5600
  2093 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152
  FEATURE:
  SEQUENCE CHARACTERISTICS:
  APPLICANT: BARR, PHILIP J.

APPLICANT: SHAPIRO, JOHN P.

APPLICANT: KIEFER, MICHAEL C.

TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE

TITLE OF INVENTION: THEREOF
   FEATURE:
  FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
   PRIOR APPLICATION DATA:
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
  61
   TELEFAX: (415
TELEX: 706141
  NAME/KEY:
LOCATION:
   LOCATION:
  STRANDEDNESS:
  CLASSIFICATION:
  FILING DATE:
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICATION NUMBER: US 08/152,443 FILING DATE: 15-NOV-1993
   CITY: Palo Alto
STATE: Californi
   ب
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   nucleic acid
  94304-1018
  LEHNHARDT, SUSAN K
   California
   3: MORRISON & FOERSTER 755 Page Mill Road
   (415) 494-0792
   Conservative
  CDS
195..1136
  mat_peptide
243
  linear
  18-MAY-1995
  single
   100.0%;
   7.0%;
   Release #1.0, Version #1.30
  US/08/444,231
  0;
  Score 226; DB 1;
Pred. No. 9.9e-53;
0; Mismatches 0;
  Length 2471;
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  Gaps
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Q
   Дb
  QΥ
  밁
  QΥ
  US-08-152-443A-18
  QΥ
   Вþ
   US-08-152-443A-18
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NAME/KEY:
   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
   SEQUENCE CHARACTERISTICS:
   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
  ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K
   COMPUTER READABLE FORM:
  STREET: /J
CITY: Palo Alto
   CORRESPONDENCE ADDRESS:
  APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS
TITLE OF INVENTION: THEREOF
  APPLICANT:
   2213 attgctcaacaaccatgctgggcatctggaccctcctacctctggt 2258
 121
  NUMBER OF SEQUENCES:
   121
   181 ATTGCTCAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGT
   61
   TELEPHONE: (415) 494-0792
  APPLICATION NUMBER: FILING DATE: 15-NOV CLASSIFICATION: 43
  NAME/KEY:
LOCATION:
  TYPE: nucleic acid
STRANDEDNESS: single
  REFERENCE/DOCKET NUMBER:
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  LOCATION:
   TOPOLOGY:
   REGISTRATION NUMBER:
  MEDIUM TYPE:
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   gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
   GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG
  226;
   CTCCCGCGGGTTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCACTTCGGAGG 180
  94304-1018
  California
   2471 base pairs
   755 Page Mill
  Conservative
   USA
  CDS
  BARR,
   mat_peptide
243
  195..1136
   linear
   MORRISON &
   Floppy disk
  15-NOV-1993
  PHILIP J.
   7.0%;
100.0%;
  SUSAN K.
   NOVEL FAS PROTEIN AND METHODS OF USE
   US/08/152,443A
   33,943
  0;
   Score 226; DB 1;
Pred. No. 9.9e-53;
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   GENERAL INFORMATION:
  REFERENCE/DOCKET NUMBER: !
INFORMATION FOR SEQ ID NO: 1:
   MOLECULE TYPE:
   ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
   CURRENT APPLICATION DATA:
  COMPUTER READABLE FORM:
  CORRESPONDENCE ADDRESS:
  APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
   2213 attgctcaaccatcctgggcatctggaccctcctacctctggt 2258
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   SEQUENCE CHARACTERISTICS:
   181
  LIKET: P.O. Box 2266 Eads Station CITY: Arlington STATE: Virginia
  NAME/KEY: mat_peptide LOCATION: 243..1199 IDENTIFICATION METHOD:
  NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD:
   TYPE: nucleic acid
  APPLICATION NUMBER: US/0 FILING DATE: 28-MAR-1994
   SOFTWARE: PatentIn Release #1.0, Version #1.25
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  NAME/KEY:
LOCATION:
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   TOPOLOGY:
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polyA_site
   Homo sapiens
  polyA_site
1831..1836
   linear
   cDNA to mRNA
  double
  US/08/219,237B
   28,808
                                    to
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  516762
  similarity with known sequence an established conserved
                                   similarity with known sequence an established consensus
   similarity with known sequence an established consensus
   similarity with known sequence or an established consensus
   or
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RESULT 5
US-08-468-560C-1
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   Дb
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  밁
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   Sequence 1, Application Patent No. 6270998
   Best Local Similarity 100. Matches 226; Conservative
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Best Local 9
   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
   APPLICANT: NAGATA, Shi
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, SI
  REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
   ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LENGTH: 2534 base pairs
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  TITLE OF INVENTION: DNA COD
MOLECULE TYPE:
   121
   TELEPHONE: /UJ ___ TELEPHONE: /UJ __ TO NO:
  APPLICATION NUMBER: US/08/468,560C FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
  ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
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  LOCATION:
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  LOCATION: 2352..2357 IDENTIFICATION METHOD:
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  22040-0747
   Application US/08468560C
  USA
   NAGATA, Shigekazu
   polyA_site
2518..2523
              linear
cDNA to mRNA
                                double
  DNA CODING FOR HUMAN CELL SURFACE
   28,977
  ьу
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  20-4393P
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  Mismatches
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  0;
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```

ORIGINAL

SOURCE:

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DЬ
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; ORGANISM: Homo sapiens
US-09-180-100-16
   US-09-180-100-16
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SOFTWARE: PATENTIN VET. 2.0
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CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
  APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
2213 attgctcaacaaccatgctgggcatctggaccctcctacctctggt 2258
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  FEATURE:
  FEATURE:
   FEATURE:
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  0;
   0;
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   В
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   , CLONE: pTZgpt-F1s
US-08-232-463-14
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US-08-232-463-14
  Š
   밁
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   DЬ
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  ΩY
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Patent No. 5670367
  INFORMATION FOR SEQ ID NO:
   FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
   GENERAL INFORMATION:
                                    APPLICANT: APPLICANT: APPLICANT: 1
   IMMEDIATE SOURCE:
   COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 7218 base pairs
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
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  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
   APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBI
  394 tttaattootgactotgotatttattaactaaccatotttgccaatgttgcttaagcttt 453
   2093 ggcactggcacggaaccaccctgaggccagccctggctgcccaggcggagctgcctctt
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   TOPOLOGY:
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  TELEFAX:
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   FILING DATE:
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   Alexandria
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  ٧A
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  (703)683-4109
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  EP 91 114 300.6
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   US/08/232,463
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  30472/114 IMMU
   Suite 500
   Version #1
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  Gaps
  2152
  0;
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  В
  US-08-232-463-14/c
   Sequence 14, Application US/08232463 Patent No. 5670367
   GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO:
  NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
   CURRENT APPLICATION DATA:
  TITLE OF INVENTION: NUMBER OF SEQUENCES:
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   APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
  CORRESPONDENCE ADDRESS
  APPLICANT:
IMMEDIATE SOURCE:
CLONE: pTZgpt-
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  574
   514 aatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataattcacac 573
   694 acatttttttatttaaatgaacttttcattttggaatagttttaggatttcaaaaaattt 753
  634 attecttecettacctetecttecetteceteacaccccetttecettecttettt 693
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   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
  CLASSIFICATION: 435
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  CITY: Alexandria
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  COUNTRY:
   ADDRESSEE:
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  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTATCTCTTTAACTACTT 1465
  GCATAGATA 1474
  22313-0299
   nucleic acid
   899149
pTZgpt-F1s
   1800 Diagonal Road, Suite
  SCHEIFLINGER, F. FALKNER, F. G.
   7218 base pairs
  USA
  (703)683-4109
   DORNER, F.
  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                linear
  single
  RECOMBINANT FOWLPOX VIRUS: 52
  US/07/935,313
   US/08/232,463
   30472/114 IMMU
  500
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  QY
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   GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
   SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
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  1082
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   1322
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  ctgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatc
  acctaacctagatttgagggcccaacaggctccagaagaaaatgtcaactgagaggaagc 1045
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  19102
   Pennsylvania
  E: Seidel, Gonda, Lavorgna Two Penn Center, Suite 1800
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  2.1%; Score 67.8; DB 1; ilarity 8.2%; Pred. No. 2.1e-08; Conservative 227; Mismatches 174;
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   IBM PS/2
   September 15,
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   ANTISENSE
OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
   MS-DOS
  T'Omasz
  US/08/306,691B
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INFORMATION FOR SEQ ID NO:

19:

No.

5734039e

TELEFAX: I

(215) 568-5549

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   US-08-306-691B-19
  Sequence 19, Application PC/TUS9306251 GENERAL INFORMATION:
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Best Local :
  Matches 115;
   TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
   NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
  SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
   TITLE OF INVENTION: Trivalent Synthesis of Carly Invention: Stereospecific Alkylphosphonates and Arylphosphonates NUMBER OF SEQUENCES: 93
   SOFTWARE: Patentin Release #1.0, Version #1.25
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
           TOPOLOGY: 15
   CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
  ATTORNEY/AGENT INFORMATION:
   APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
   3986 TTCTTTCTTTTTCTATCTTTTGAGA 4012
   3866
  3806 GAGGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTAGGCGACAGAGCAAGACT 3865
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  Qy
   Qγ
   В
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APPLICATION NUMBER: USSN
FILING DATE: 23 DEC-1994
INFORMATION FOR SEQ ID NO: 9
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LENGTH: 857 base pairs
TYPE: nucleic acid
Grap NUTERIST.
   Sequence 7, Application PC/TUS9517083 GENERAL INFORMATION:
   Query Match
Best Local
   Sequence 9, Applicati
GENERAL INFORMATION:
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   Query Match
Best Local Similarity
Matches 115; Conserv
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APPLICATION NUMBER: 1
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  2202 cacttoggaggattgotcaacaaccatgotgggcatctggaccctcctacctactggt 2258
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   3806
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   714 acttttcattttggaatagttttagga 740
  534 gaagatccacatatgtgagttgctggcttataattcacactcaagagatactgattttgt 593
  CLASSIFICATION:
  STRANDEDNESS:
                TYPE:
   FILING DATE:
   FILING DATE:
  APPLICATION NUMBER:
                            LENGTH:
  1 CACTTCGGAGGATTGCTCAACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGT 57
  STRANDEDNESS: single
  FILING DATE: C
CLASSIFICATION:
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  GAGGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTAGGCGACAGAGCAAGACT 3865
  ch 1.8%; Score 57; DB 1 Similarity 100.0%; Pred. No. 5.: 57; Conservative 0; Mismatches
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   23-DEC-1994
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  CONCURRENTLY HEREWITH
   CONCURRENTLY HEREWITH
   23-DEC-1994
  1.9%;
   SECRETED HUMAN FAS ANTIGEN
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   USSN 08/371,263
  PCT/US95/17083
   USSN 08/371,263
   PCT/US95/17083
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  ; DB 5; L., 10. 5.3e-06; 0;
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δÃ
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  PCT-US95-17083-5
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   PCT-US95-17083-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
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Query Score Match Length DB

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Description

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Sequence 1, Application US/09834291

Sequence 1, Application US/09834291

APPLICANT: Krammer, Peter

APPLICANT: Muller-Schilling, Martina
APPLICANT: O'ren, Moshe
FITTLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122

CURRENT PILING DATE: 2001-08-21

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: PCT/DE99/0343

PRIOR FILING DATE: 1999-10-18

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PRIOR FILING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.1

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  APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
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CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
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| c 2219                                                               | c 2159<br> <br>c 10153 | g 2099<br> <br>g 10093                                        | t 2039<br> <br>  t 10033                                             | rc 1979<br> <br> c 9973 | jc 1919<br>                                                           | cc 1859                                                             | gc 1799<br>  <br>gc 9793                                            | aa 1739<br>                                                     | gc 1679<br>  <br> gc 9673                                           | ag 1619<br>  <br>ag 9613                                              | ac 1559<br>  <br>ac 9553 | tt 1499<br> | tg 1439<br> | at 1379<br>  <br>at 9373 | .gt 1319<br>  <br>.gt 9313 | tt 1259<br>  <br> tt 9253 | gaa 1199<br>   <br> gaa 9193                                       | gt 9133                                                           |

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| C 87                          |                                                                   | U    | Ъ    |
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Application

US/09834291

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PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Ma
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding
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                                                                                                                                                                                                                                                                                                                                                                                       | 2209 | cgg 2                     | 2209    | 999 2519                                                          | 2209    | acg 2459                                                           | 2209    | ıggc 2399                                              | 2209           | tgc 2339                                                      | 2187    | ggtg 2279                                                        | 218 | tgctc 2219                        | <br>                                                | cccgc 2159                                            | [  <br> <br>  ctg 210 | ctq 209                        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DP QA

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APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated
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| 1765 | cctccccaacttcccaggttgaactacagcagaagcctttagaaagggcaggaggaggccggc | 1706 | QY       |
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| N    | cttgagaaataaaaactaaggggccctcccttttcagagccttatggcgcaaca          |      | ОУ       |
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| 660  | ctgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatc    |      | Дb       |
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| 8    | tggcactaacagtctactgaaaggtggaacagagacaagcctatcaacacctacaagact    |      | фd       |
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Sequence 94, Application US/09802669
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Wyatt, Jacqueline
FILTE OF INVENTION: Antisense Compound Modulation of
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/660,619
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
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PRIOR APPLICATION NUMBER: PCT/DE99/0343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, William J
APPLICANT: Zhou, Tong
TITLE OF INVENTION: Human Tong
  GENERAL INFORMATION:
  NAME: Sertich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UOAB
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TELEFAX: 512/474-7577
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FILING DATE: 20-JAN-1995
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OPERATING SYSTEM: MacIntosh
SOFTWARE: MICICOSOft Word for Macintosh
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FILING DATE: January 20, 1995
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
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  TELEPHONE: (713) 777-2321
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  NAME: Benjamin Aaron Adler, Ph.D., REGISTRATION NUMBER: 35,423
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TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Lal, Preeti
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CURRENT EILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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   US-09-404-284-674
  Sequence 674, Application US/09404284
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
  SEQ ID NO 674
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Best Local
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CURRENT APPLICATION NUMBER: US/09/404,284
CURRENT FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
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ORGANISM: Homo
   LENGTH: 449
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  1919
   1739
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   421
  449 CGTTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAACTACAGCAGA 390
  209
  329
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  ccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctggggttggtgg
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  agcctttagaaagggcaggaggccggctctcgaggtcctcacctgaagtgagcatgccag 1798
 ggcacggaa
                               TCTGGGGAGTGAGGAAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGCACT
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  Gaps
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GGCACGGGA

US-09-524-038-674/c

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US-60-324-185-9888/c; Sequence 9888, Application US/60324185; GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-03-13
CARLIER APPLICATION NUMBER: 09/404,284
EARLIER FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 674
LENGTH: 449
CORGANISM: Homo Sapiens
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  US-09-524-038-674
   Sequence 674, Application US/09524038
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee w.
APPLICANT: MORTIS, MACDONALD
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
   Query Match
Best Local Sim
Matches 426;
   TITLE OF INVENTION: Novel Nucleic Acid Sequences TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 780CIP
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   CCCTCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCCTGACCACCGGGG
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  0;
   210
  270
   150
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  0;
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RESULT 15
US-09-644-867-7725/c
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  NAME/KEY: unsure
LOCATION: 1156, 1235, 1267, 1304,
THER INFORMATION: a, t, c, g, or
US-60-324-185-9888
   Sequence 7725, Application US/09644867 GENERAL INFORMATION:
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7725
  APPLICANT: Holtzman, Douglas A.
APPLICANT: Donovan, Michael J.
APPLICANT: Leiby, Kevin R.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1173-001
CURRENT APPLICATION NUMBER: US/09/644,867
CURRENT FILING DATE: 2000-08-28
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Incyte ID No: 1383957.6
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TYPE: DNA
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  2349
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US-09-644-867-7725

Search completed: September 7, 2002, 22:30:49 Job time: 43743 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Perfect score:
   OM nucleic - nucleic search, using sw model
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  DB
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             252
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67.8
60.8
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6: /cgn2_6/ptodata/2/pna/U
8: /cgn2_6/ptodata/2/pna/U
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Match
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  September 7, 2002, 14:52:02; Search time 1826.34 Seconds (without alignments) 5355.992 Million cell updates/sec
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  Gapop 10.0 , Gapext 1.0
   IDENTITY_NUC
   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
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US-10-113-906-21
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US-10-035-832-1263
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US-10-113-872-1669
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Sequence 471, App
Sequence 477, App
Sequence 21, Appl
Sequence 9394, App
Sequence 1263, Ap
Sequence 143, App
Sequence 133, App
Sequence 1259, Ap
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   RESULT 1
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   301 gaacttgaggataattagacgtacgtgggtagagggtaggggaagggggtatggcataga 360
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| 4444                                                                                                         | 000                                                                                 | C 34<br>3634                                                                         | 3333                                                                           | 2222                                                                                       |
|--------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|--------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| 01 = 00 10 =                                                                                                 | -000                                                                                | ~ 0101 <del>-</del>                                                                  |                                                                                |                                                                                            |
| 53.8<br>53.8                                                                                                 | 54.4                                                                                | 554.50<br>54.60<br>54.60                                                             | 55.2<br>54.8<br>54.8                                                           | 555.<br>55.<br>88.                                                                         |
|                                                                                                              |                                                                                     |                                                                                      |                                                                                |                                                                                            |
| 1.7                                                                                                          | 1.7                                                                                 | 1.7                                                                                  |                                                                                | 1.7<br>1.7<br>1.7                                                                          |
| 2759<br>27827<br>27827<br>375<br>375                                                                         | 1076<br>44990<br>44990                                                              | 1527<br>2501<br>48763<br>551                                                         | 443<br>443<br>1191139<br>1191139                                               | 1140<br>1140<br>443<br>443                                                                 |
| 1167                                                                                                         | n on on on ·                                                                        | 7 1 7                                                                                | 7<br>7<br>7                                                                    | 7                                                                                          |
| US-10-027-632-111688<br>US-10-035-832-1328<br>US-10-035-832-1328<br>PCT-US02-09239-329<br>PCT-US02-09239-331 | US-10-098-754-1296<br>US-10-035-832-1229<br>US-10-052-832-1229<br>US-10-052-482-217 | US-10-011-154-202<br>US-10-027-632-103140<br>PCT-US02-23268-3<br>US-10-027-632-71673 | US-10-027-632-296990 US-10-027-632-296991 US-09-811-352B-1 US-10-140-924-1     | US-10-027-632-253750<br>US-10-027-632-253751<br>US-10-027-632-64316<br>US-10-027-632-64317 |
| Sequence 111688, Ap<br>Sequence 1328, Ap<br>Sequence 329, App<br>Sequence 331, App                           | 129<br>1229<br>217                                                                  | Sequence 202, App<br>Sequence 103140,<br>Sequence 3, Appli<br>Sequence 71673, A      | Sequence 296990,<br>Sequence 296991,<br>Sequence 1, Appli<br>Sequence 1, Appli | Sequence 253750,<br>Sequence 253751,<br>Sequence 64316, A<br>Sequence 64317, A             |

## ALIGNMENTS

Minimum

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PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PAtentin version 3.1
SEQ ID NO 1262
LENGTH: 45121
TYPE: DNA
  Query Match
Best Local Similarity
Matches 3207; Conserv
   APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT EILING DATE: 2002-07-22
  PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
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  Conservative
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99.8%; Pred. No. 0;
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  5; Indels
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| Db<br>Qy<br>Db                            | 0 Db Qy Db                                                     | 24<br>24<br>25<br>26<br>27<br>27                                                                                                                                                 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                         | 24<br>24<br>25<br>25<br>26<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27                                                              |
|-------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 466                                       | 2160<br>10154<br>2220<br>10214<br>2280<br>10274                | 91.98                                                                                                                                                                            | 174<br>173<br>179<br>179<br>186<br>186                        | 937 <i>i</i><br>1440<br>9434<br>1500<br>9494<br>1560<br>9554<br>1620<br>9614                                                                                          |
| 1                                         | ggyttggtggacccgctcagtacggagttggggaagctctttcacttcggaggattgctc 2 | cctccccaacccgggcgttccccagcgaggcttccttcccatcctcctgaccaccgggc gtttccccaacccgggcgt tttttcgtgagctcgtcttgatctcgcgcaagagtgaccaccagggtgttcaaagacgctt llllllllllllllllllllllllllllllllll | gcetttagaaaggcaggaggccggctctcgaggtcctcacctgaagtgagcatgccagc 1 | 4 gagtaacgaaggacaggaagtaattgtgaatgtttaatatagctggggctatgcgatttg of gettaagttgttagctttgttttcetettgagaaataaaaactaaggggccetecettt lillillillillillillillillillillillillil |
| 5 1 3 9 3 9 3 1 1 9 9 9 9 9 9 9 9 9 9 9 9 |                                                                | 973<br>039<br>0033<br>0099<br>0093<br>159                                                                                                                                        | 7 1 1 5 5 6                                                   | 499<br>499<br>9493<br>559<br>553<br>619<br>613<br>679<br>673<br>739                                                                                                   |

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|--------------|--------------------------------------------------------------------------|--------------|----------|
| 2            | agtaacgaaggacaggaagtaattgtgaatgtttaatatagctggggctatgcgatttg              | 1380         | Qγ       |
| 9373         |                                                                          | 31           | D .5     |
| 3            | atgctaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagtgt              | 9254         | g g      |
| 1319         | catyctaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagtgt :           | 26           | Qy       |
| 25           | ctgcatccaaattcaggttcagtaatgatgtcattatccaaacattaccttctgtaaaatt            | 9194         | рb       |
| 25           | Tycatccaaattcaggttcagtaatgatgtcattatccaaacataccttctgtaaaatt              | 1200         | Qy       |
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| 9133         | taatgtgttattaatgggttgaatctaattgggaagggagagaggttgcagagtgaggt              |              | дь       |
| 1139         | tgtgttattaatgggttgaatctaattgggaagggagagaggttgcagagtgaggt                 | 1080         | ρ        |
| 9073         |                                                                          | 01           | 망        |
| 2 01         | tyatgyaaagcctcaggagggtaacctaacctagatttgagggcccaaacaggctcca               | 1020         | 0 6      |
| 1019         | 9tgatggaagccctcaggagggtaacctaacctagatttgagggccc-aacaggctcca              | 96           | VQ.      |
| 8953         |                                                                          |              | 망        |
|              |                                                                          | 901          | Q<br>Q   |
| 900          | gyctygcacycccayyytcttcctcatyycactaacagtctactgaaaggtggaacagag<br>         | 841<br>8834  | ρ Q      |
| 8833         | taccatccttattcccacttcttttgtgtctattagatgctcagagtgtgtgcacaa                | 7            | дь       |
| 840          | taccatcctccttatcccacttcttttttgtgtctattagatgctcagagtgtgtgcaca             | 781          | Qγ       |
| 7            |                                                                          | 8714         | Db       |
| œ            | ttttggaatagttttaggatttcaaaaaatttgcagagataatacagagaatgcccat               | 721          | Qy       |
| 720<br>8713  | cttccctcacaccccttttccttccttcttttacatttttt                                | 661<br>8654  | dd<br>So |
| 8653         | actttcccctttttttctctcttccctccttccattccttctt                              | 8594         | Dβ       |
| 660          | cotttoccettttttttctctcttccctccttccattccttccttc                           | 601          | Qγ       |
| UI .         |                                                                          | 8534         | ДD       |
| 00           | acatatgtgagttgctggcttataattcacactcaagagatactgattttgtcaattg               | 54           | γQ       |
| Ċι,          |                                                                          | 7            | Ъ        |
| 4            | taagtttaataatcactcatctcactgggctataatgataagtattaagtaag                    | 481          | Qγ       |
| 4            | act                                                                      | <b></b>      | Д        |
| ω .          | actaaccatctttgccaatgttgcttaagctttttttggctacatttttttattataa               | 421          | VΩ       |
| 420<br>8413  | <pre>l aagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatttatt</pre> | 8354         | ₽ Q      |
| 8353         |                                                                          | 9            | D        |
|              |                                                                          |              |          |

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  RESULT 2
US-10-011-154-674/c
CURRENT APPLICATION NUMBER: US/10/011,154
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13 |
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21 |
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 674
  Sequence 674, Application US/10011154 GENERAL INFORMATION:
  APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee w.
   TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 780CIP
  10514
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  10634
  10574
  10934
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  2580
  2520
  3060
  2880
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  cagaaatgccagcttgcagatggctaatcaaag 3212
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  ccatggtgatttctgcttggtctcctgctggtggtttggtggtactcgttcccaccgcacag 3119
  cattttgtttttttctgcccttctctttcttctttttgccctttcttagcctc
  gccttgtctcccttccgggaattctctctttaagactgtaagtcgctgcctgagtggttt
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  agatattgctcattttctggcagttctcagacgtaggaaataagtcagcaccgaagcagt
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  10633
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; ORGANISM: Homo sapiens US-10-011-154-674
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US-10-211-364-477
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  PRIOR APPLICATION NUMBER: 09/760,486
PRIOR FILING DATE: 2001-01-16
PRIOR PPLICATION NUMBER: 60/7179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR PPLICATION NUMBER: 60/214,886
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PRIOR PPLICATION NUMBER: 60/217,487
PRIOR PPLICATION NUMBER: 60/217,487
PRIOR PPLICATION NUMBER: 60/227,787
PRIOR PILING DATE: 2000-07-11
PRIOR PPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
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  Sequence 477, Application US/10211364 GENERAL INFORMATION:
   Matches 426;
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   APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins,
   FILE REFERENCE: PJZ16C1N
Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1778
                          PRIOR FILING DATE: 2000-07-14
  1979
  1859
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   CTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCT
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  Similarity
   Conservative
   13.2%;
  0;
   Score 424.2;
Pred. No. le-
  Mismatches
  1e-80;
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  and
                  File
  ω
  7;
  Length
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                   PALM
   Gaps
  1978
   1918
   1858
  270
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   90
  150
   0,
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Q
   WESULT 4
US-10-143-906-21
   B
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   ; OTHER INFORMATION: n equals US-10-211-364-477
   Sequence 21, Application US/10143906
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ70CIN
CURRENT APPLICATION NUMBER: US/10/143,906
CURRENT FILING DATE: 2002-05-14
   Prior Application removed -
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 772
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LENGTH: 772
   NAME/KEY: misc_feature
LOCATION: (593)
OTHER INFORMATION: n equals
FEATURE:
   ORGANISM: Homo sapiens FEATURE:
FEATURE:
       OTHER INFORMATION: n equals a,t,g,
                        NAME/KEY: misc_feature LOCATION: (594)
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  FEATURE:
NAME/KEY: misc_feature
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  NAME/KEY: misc_feature LOCATION: (704)
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  1983
   309
  249
  129
   69
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  ttggtggacccgctcagtacggagttggggaagctctttcacttcggaggattgctcaac 2222
   cggaacacaccctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggg 2162
  aaccatgctgggcatctggaccctcctacctctggt 344
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   tcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacgcttctg 128
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  (594
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  a,t,
  a,t,g,
  a,t,g,
   0;
  Score 334.4; DB 6
Pred. No. 1.8e-61;
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; Sequence 85, Application PC/TUS0210824
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APPLICANT: OFIGENE Technologies
TITLE OF INVENTION: Prostate Cancer Expression Profiles
: FILE REFERENCE: 9U 206 PCT
: CURRENT APPLICATION NUMBER: PCT/US02/10824
: CURRENT FILING DATE: 2002-04-08
: PRIOR APPLICATION NUMBER: US 60/281,732
: PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/281,731
: PRIOR APPLICATION NUMBER: US 60/281,731
: PRIOR FILING DATE: 2001-04-06
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   Db
  Qy
  В
   PCT-US02-10824-85
   PCT-US02-10824-85
  Q
  B
   Ωy
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   Qy
   밁
  Qу
  DЪ
   Qy
  Дb
  ; NAME/KEY: misc_feature
; LOCATION: (704)
; OTHER INFORMATION: n equals a,t,g,
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   NUMBER OF SEQ ID NOS: 211
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.0%;
  Matches 252;
  Matches 335;
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ORGANISM: Homo sapiens
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  121
   2163
  1983 tcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacgcttctg 2042
   189
  309
  249
   129
   61
  69
   \vdash
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  9 cgccaacccgggcgttccccagcgaggcttccttcccatcctcctgaccaccggggcttt 68
tggctgcccaggcggagctgcctcttctcccgcgggttggtggacccgctcagtacggag
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  gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc
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   ttggtggacccgctcagtacggagttggggaagctctttcacttcggaggattgctcaac
   aaccatgctgggcatctggaccctcctacctctggt 344
  ttggtggacccgctcagtacggagttggggaagctctttcacttcggaggattgctcaac
   cggaacacacctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggg
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99.7%;
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  Indels
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  120
  60
  188
   248
  2162
   2102
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   PCT-US02-25766-9394
  RESULT 7
US-10-035-832-1263
  밁
  Qy
  PCT-US02-25766-9394
  CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE PATENTIN VET: 2.1
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   Sequence 1263, Application US/10035832
  Matches
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  APPLICANT: GENE LOGIC, INC. APPLICANT: MUNGER, William
               APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
  APPLICANT:
   APPLICANT:
  TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5068-WO
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  APPLICANT:
PRIOR APPLICATION NUMBER: US 09/747,377
  FEATURE: OTHER INFORMATION: Genbank Accession No. X63717
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ORGANISM: Homo sapiens
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   241 cctacctctggt 252
   61
  \vdash
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  tggctgcccaggcggagctgcctcttctcccgcgggttggtggacccgctcagtacggag 180
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  9394, Application PC/TUS0225766
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   MUNGER, William E
FAULK, Ronald
SUN, Hongwei
SASAI, Hitoshi
  YAMAMOTO, Jun
   WAGA, Iwao
  Conservative
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100.0%; Pred. No. 9.4e-44;
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US-10-007-926A-143
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   ; TYPE: DNA; ORGANISM: Homo sapiens US-10-035-832-1263
  US-10-007-926A-143; Sequence 143, Application US/10007926A
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   QΥ
   Вb
   QY
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LENGTH: 2551
   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 143
LENGTH: 2551
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   Query Match
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   Query Match
Best Local Similarity
  PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PatentIn version 3.1
  APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
  PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
   CURRENT APPLICATION NUMBER: US/10/007,926A CURRENT FILING DATE: 2001-12-07
  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES FILE REFERENCE: 1546-R-00
  PRIOR APPLICATION NUMBER: 60/254,090 PRIOR FILING DATE: 2000-12-08
   APPLICANT: BERTUCCI, FRANCOIS
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2007 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 2066
  2127
  2067
  2007 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 2066
  121
   241 cctacctctggt 252
   61
  y Match 7.8%; Score 252; DB 6;
Local Similarity 100.0%; Pred. No. 9.4e-44;
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   gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
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CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 233
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TYPE: DNA
ORGANISM: Homo sapiens
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  GENERAL INFORMATION:
  Sequence 233, Application US/09053375B GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
          CURRENT APPLICATION NUMBER: US/10/035,832 CURRENT FILING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-02
  Query Match
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   APPLICANT: MOTTIS, David
APPLICANT: MOTTIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: MOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71249/RMS/DCF
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  121
   2067
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   241 cctacctctggt 252
   61
   Local Similarity
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  61
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  cctacctctggt 2258
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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   7918 gacttctctttt
  7859 aag-gaggaagtaataatgtctaacacagcaggtgagggttttcccttttactgaaaata 7917
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   1329
   7739
  LENGTH:
   gttagctttgttt 1461
  aggacaggaagtaattgtgaatgtttaatatagctggggctatgcgatttggcttaagtt 1448
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  128;
  55996
  Conservative
   Application US/10027632
  7930
   2.1%;
  at positions
   at positions
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  positions
  positons 46987
  0;
  Score 67.8; DB 6;
Pred. No. 0.00046;
0; Mismatches 62
   55549 thru
   53136 thru
  50692 thru
  48271 thru
   42691 thru
  thru
  47006
   55568
   53155
  50711 can
  48290
   42710
   31239
   Length 55996;
  Indels
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  base
   Gaps
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  ; TYPE: DNA; Homo sapiens US-10-113-872-796
   밁
RESULT 13
   US-10-113-872-796/c
   ; TYPE: DNA; Human; ORGANISM: Human US-10-027-632-145670
   PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR ETLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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   APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
   NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
   APPLICANT:
  APPLICANT:
  APPLICANT: Watanabe, Yoshihiro APPLICANT: Henderson, Robert
  APPLICANT:
   NUMBER OF SEQ ID NOS: 325720
  LENGTH: 2435
  LENGTH: 816
  247 AAGATAGTACAGAAAATTCCCCACATACTGCACACCGTTTCCCCCTGTTTTTAACATTTTAT 188
  757 gagataatacagagaatgcccatatacccatcctccttatcccacttctttttgtgtctat 816
   307 TGTTTTTGTTTAAATAAACTTTTGCTTTTAGAACAGTTTTAGCTC,TACAGAATTATTGCA 248
   697 tttttttatttaaatgaacttttcattttggaatagttttaggatktcaaaaaatttgca 756
  Local Similarity es 81; Conserv
  Match 1.9%; Local Similarity 69.2%;
  APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20
  83;
   Henderson, Robert A
Kalos, Michael D.
Sleath, Paul R.
Vedvick, Thomas S.
  Conservative
  Conservative
   1.9%;
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; ORGANISM: Human US-10-027-632-91808
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  US-10-113-872-1669/c
   SOFTWARE: FASTSEQ for Windows Version 4.0
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LENGTH: 542
TYPE: DNA
  Sequence 91808, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1669
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  Query Match
Best Local
  GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
  NUMBER OF SEQ ID NOS:
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PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
  FILE REFERENCE: 108827.129
  APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
  NUMBER OF SEQ ID NOS: 2011
  APPLICANT:
APPLICANT:
   APPLICANT:
  APPLICANT:
  APPLICANT: Watanabe, Yoshihiro
  LENGTH: 2821
   2734 TAGATTTACAGAGAAGTTGCAGAGATAGTACAAAGAGTTCCTGTATACCCTTCACC 2679
   736 taggatttcaaaaaatttgcagagataatacagagaatgcccatataccatcctcc 791
  676 tittccttccttcttttacattttttatatttaaatgaacttttcattttggaatagttt 735
   Y Match 1.9%;
Local Similarity 69.8%;
   81;
   Sleath, Paul R. Vedvick, Thomas S.
  Henderson, Robert
Kalos, Michael D.
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   Robert A.
   0; Mismatches
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Best Local Similarity Matches 70; Conserv

Conservative

1.8%; Score 59.2; DB 7; 79.5%; Pred. No. 0.0081; ative 0; Mismatches 18;

DB 7; Length 542;

0

0;

Query Match

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US-10-027-632-304597
Sequence 304597, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION. Identification and Mapping of Single Nucleotide
TITLE OF INVENTION. Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-07-12
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 304597
LENGTH: 542
TYPE: DNA
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Search completed: September Job time: 37034 sec
   밁
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; ORGANISM: Human
US-10-027-632-304597
   Query Match 1.8%; Score 59.2; DB 7; Length 542; Best Local Similarity 79.5%; Pred. No. 0.0081; Matches 70; Conservative 0; Mismatches 18; Indels
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  44 ttgttttatttaaatgaacttttaattttagaatagttttacagttacagagaagttgca 103
                            8
                            2002, 01:09:16
   Gaps
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Minimum DB
Maximum DB
   Total number of hits satisfying chosen parameters:
   Scoring table:
  Title:
Perfect score:
  OM nucleic - nucleic search, using sw model
  Database
  Post-processing: Minimum Match 0%
   Result
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
276.4
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340.6
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   EST:*
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2: em,
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6: em
6: em
7: er
8: er
9: g
110:
113:
114:
115:
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22.1
114.1
12.0
112.0
10.6
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8.7
7.9
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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793
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|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|------|----|------|--------------------|-------|-------------------|--------------------|----------|-------------------|-------------------|--------------------|----------|----------|-------------------|--------------------|----------|-----------------------------------------|
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|                    |                    |                    |                    |                    |                    |                    |                    |          |          |          |      |    |      |                    |       |                   |                    |          | 696 9             |                   |                    |          |          |                   |                    |          |                                         |
|                    | CNS0165X           |                    | CNS0182P           | BG076530           | AA521406           | AA521324           | AA668797           | CNS016J7 | CNS0072Q | CNS01523 |      |    |      |                    | D     | AA383161          | BM310113           | в1838027 | AV715411          | R85827            | BI463384           | BM455788 | AU100132 | AL542093          | BG288747           | AV692383 | 1000144                                 |
| AL106663 Drosophil | AL106335 Drosophi. | AZ184604 SP_1003_F | ALIUSUII Drosophii | BG076530 H3001D05- | AA521406 aa68C09.S | AA521324 aa68e09.s | AA668797 aa80dll.s | Drosop   |          |          |      |    |      | BM090262 505440 MA |       | AA383161 EST96716 | BM310113 ihiihii.y | 6030838  | AV715411 AV715411 | R85827 yq22g10.s1 | BI463384 603204413 |          |          | AL542093 AL542093 | BG288/4/ 502385555 | AV692383 | 1000000 1000000000000000000000000000000 |

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## ALIGNMENTS

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KEYWORDS
SOURCE
  ACCESSION
VERSION
  COMMENT
  FEATURES
   REFERENCE
   DEFINITION
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B1763679/c
  LOCUS
   AUTHORS
TITLE
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   JOURNAL
  source
  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11474 row: e column: 17
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
  B1763679 793 bp mRNA linear EST 25-SEP-20
603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
  High quality sequence stop: 786.
Location/Qualifiers
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  EST
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  BI763679
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/lab_host="DH10B"
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  /organism="Homo sapiens"
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  linear
   EST 25-SEP-2001
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  BASE COUNT
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  2381 gcgggctgctgcgggaggcgttggagacttgctcccggggggctgttaggaccttccctca 2440
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  496
   792 CCCCCTCCTGCCGG--TGAGGCTTACCCCGTCTTATTCCC-GGGATAGGCAAAGT-GGG 737
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   CAGGGCTGCTGCGGAGGCGTTGGAGACTGGCTCCCGGGGGCTGTTAGGACCTTCCCTCA
  AGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAAT
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   destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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 mRNA
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  6,
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   FEATURES
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  VERSION
   DEFINITION
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JOURNAL
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   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 459.
  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 467)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU,NCI human EST Project
  zj19h02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450771 3', mRNA sequence.
  Tel: 314 286 1800
Fax: 314 286 1810
  Contact: Wilson RK
  Unpublished (1997
  Homo sapiens
  AA704610.1 GI:2714528
   146
   Conservative
   Ω
   constructed by Bento Soares and M.Fatima Bonaldo." 82 c 121 g 118 t
  and Eco RI sites of the modified pT7T3 vector. I went through one round of normalization. Library
  /dev_stage="20 week-post conception fetus"
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                         993
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  REFERENCE
AUTHORS
   SOURCE
ORGANISM
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  COMMENT
  KEYWORDS
  VERSION
  DEFINITION
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   ACCESSION
  Cocus
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   1113
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  2349
   301
   994
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  361
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   397;
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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  Genoscope - Centre National de Sequencage
   Contact: Genoscope
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(bases 1 to 899)
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   91006 EVRY cedex - France segref@genoscope.cns.fr, V
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   fliang@lifetech.com URL:
http://fulllength.invitrogen.com"|
http://fulllength.invitrogen.com"|
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   TgESTzya24g01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplasma go cDNA clone TgESTzya24g01.y1 5′ similar to TR:063030 Q63030 RAT ALPHA-SMOOTH MUSCLE ACTIN MRNA FRAGMENT ;, mRNA sequence EG659530
  Contact: Clifton, S.
Contact: Clifton, S.
Toxoplasma EST Project
Toxoplasma EST Project
Washington University School of Medicine
   Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
   Contact David Sibley (toxest@borcim.wustl.edu) information relating to organism, libraries, or seg primer: -40RP from Gibco High quality sequence stop: 371.
  4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
  Toxoplasma
  Toxoplasma gondii.
   Email: toxo@watson.wustl.edu
  Unpublished (2001)
  Toxoplasma EST Project
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86 a
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  gondii
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  GCGGCAGCGCGCACCCTGGGCAGCCGGCGGCTGCTGCGGGAGGCGTTGCAGAC
   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Linehan
   found through the I.M.A.G.E. Consortium/LINL http://image.llnl.gov plate: LCML184 row: c column: 10 High quality sequence stop: 595.
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National Institutes of Health, Mammalian
Unpublished (1999)
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  Email: cgapbs-r@mail.nih.gov
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1 (bases 1 to 1140)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                    351 Guo Shoujing Road, Zhangjiang Hi-Tech
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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Note: this is a NIH_MGC Library." |
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  603 bp zf55b04.sl Soares retina N2b4HR IMAGE:380815 3', mRNA Semicono
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 to 603)
   This clone is available at CHGC Location/Qualifiers
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   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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  122
                314 286 1800
314 286 1810
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est@watson.wustl.edu
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 Parsons, J.,
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Db QY В Qy 밁 QУ ρ 밁 Š 멍

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Contact: Wilson RK
  Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
  IMAGE Consortium (info@image.llnl.gov)
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   Fax: 314 286 1810
   Tel: 314 286 1800
  Washington University School of Medicine
   133
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  double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
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   δÃ
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   ORGANISM
   AUTHORS
   TITLE
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  Email: est@watson.wustl.edu
  Contact: Wilson RK
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D 04

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1 GTCNCACAGAAAAAAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTNGT 60

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VERSION
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JOURNAL
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Seg primer: mob.REGA+ET
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This clone is available royalty-free through LLNL; contact the
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Fax: 314 286 1810
  Washington University School of Medicine
   Unpublished (1995)
Contact: Wilson RK
   The WashU-Merck EST Project
   ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
  1 (bases 1 to 442)
Hillier, L., Clark, N., Dubuque, T., Elliston, K.,
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1 107 c 103 g 138 t
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   SOURCE
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   DEFINITION
  TITLE
JOURNAL
   AUTHORS
   ORGANISM
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   3099
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  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
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   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
  Unpublished (1995
  ,R., Williamson,A., Wohldman
The WashU-Merck EST Project
  Contact: Wilson RK
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//lbb/host="DH10B" (amploillin resistant) (alternative resistant) (alternative resistant) (alternative resistant removal. The retina RNA was extracted for resistant removal. The retina RNA was kindly provided by Roderick R. McInnes M. D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                   95
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  VERSION
  DEFINITION
   ACCESSION
  LOCUS
  JOURNAL MEDLINE
  Query Match
Best Local S
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   ORGANISM
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  3040
   2920 gtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttttaagactgta
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   121 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTAGCTTGGTCTCCTGCTGGGGTTGGTG
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   Local Similarity
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Hillier L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Molfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.,
Generation and analysis of 280,000 human expressed sequence tags
  Tel: 314 286 1800
Fax: 314 286 1810
   Washington University School
4444 Forest Park Parkway, Box
   Contact: Wilson RK
  97044478
   Genome Res. 6 (9), 807-828 (1996)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 376)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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IMAGE:222568 3', mRNA sequence.
H84298
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Source: IMAGE Consortium, LLNL;
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 881 Std Error: 0.00
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  Tel: 314 286 1800
Fax: 314 286 1810
  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Unpublished (1995)
Contact: Wilson RK
  ,R., Williamson,A., Wohldmar
The WashU-Merck EST Project
  Email: est@watson.wustl.edu
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99.6%;
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   further information
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H84298 RESULT

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COMMENT

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COMMENT
   RESULT
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   KEYWORDS
   VERSION
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   BASE COUNT
  COCUS
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                         Unpublished (1995)
Contact: Wilson RK
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Washington University School of Medicine
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Email: est@watson.wustl.edu
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ORIGIN

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Copyright (c) 1993 - 2000
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Sequence 17, Appl
Sequence 27, Appl
Sequence 27, Appl
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Sequence 27, Appl
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Sequence 3153, Ap
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|----------------------------------------|-------------------|-------------------|-------------------|--------------------|--------------------|---------------------|-------------------|-------------------|--------------------|----------------------|-------------------|-------------------|--------------------|-------------------|---------------------|---------------------|---------------------|---------------------|
| <b>44</b><br>5                         | 43                | 42                | 41                | 40                 | 39                 | 3<br>8              | 37                | 36                | 35<br>5            | 34                   | ω<br>ω            | 32                | 31                 | 30                | 29                  | 28                  | 27                  | 26                  |
| 30.6                                   | 30.8              | 30.8              | 30.8              | 30.8               | 30.8               | 30.8                | 30.8              | 31                | 31                 | 31                   | 31                | 31.2              | 31.2               | 31.2              | 31.4                | 31.6                | 31.6                | 31.8                |
| 24.5<br>24.2                           | 24.6              | 24.6              | 24.6              | 24.6               | 24.6               | 24.6                | 24.6              | 24.8              | 24.8               |                      |                   | 25.0              |                    | 25.0              | 25.1                | 25.3                | 25.3                | 25.4                |
| 2056<br>17235                          | 16000             | 5055              | 5054              | 5054               | 5054               | 1062                | 1062              | 1891              | 1374               | 790                  | 517               | 1552              | 1371               | 643               | 502                 | 2439                | 1748                | 421                 |
| ი თ                                    | ш                 | ۲                 | 7                 | 7                  | ب                  | υī                  | 4                 | 9                 | ຫ                  | 7                    | 6                 | μ                 | σ                  | Ц                 | σ                   | σ                   | _                   | Çī                  |
| US-10-291-255-206                      | PCT-US02-22630-12 | PCT-US02-22630-3  | US-10-172-118-445 | US-10-007-926A-428 | PCT-US02-18947-445 | US-09-053-375B-1377 | US-08-134-231B-33 | US-10-205-267-2   | US-09-919-002-4023 | US-10-027-632-169978 | US-10-205-267-4   | PCT-US02-25107-37 | US-10-198-846-9726 | PCT-US02-25107-20 | US-09-918-995-32522 | US-10-198-846-13296 | PCT-US02-25766-8269 | US-09-721-544-21692 |
| Sequence 70, Appr<br>Sequence 206, App | Sequence 12, Appl | Sequence 3, Appli | Sequence 445, App | Sequence 428, App  | Sequence 445, App  | Sequence 1377, Ap   | Sequence 33, Appl | Sequence 2, Appli | Sequence 4023, Ap  | Sequence 169978,     | Sequence 4, Appli | Sequence 37, Appl | Sequence 9726, Ap  | Sequence 20, Appl | Sequence 32522, A   | Sequence 13296, A   | Sequence 8269, Ap   | Sequence 21692, A   |

## ALIGNMENTS

```
APPLICANT: MORFIS, David
APPLICANT: MORFIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2011-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEQ ID NO 1262
LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-10-035-832-1262
RESULT 2
PCT-US02_25766-3153
PCT-US02_25766
; Sequence 3153, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
   US-10-035-832-1262
  밁
  Qy
   Sequence 1262, Application US/10035832 GENERAL INFORMATION:
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   10494 gatcccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgtt 10553
  10554 gaggtgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 10613
  10614 tggag 10618
   121 tggag 125
  61 gaggtgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
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   100.0%; Score 125; DB 6; ilarity 100.0%; Pred. No. 3e-22; Conservative 0; Mismatches 0;
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  밁
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; LOCATION: (212)..(3988)
US-10-018-407A-1
                  PCT-US02-23766-55/c
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   Ş
   В
  NUMBER
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  PCT-US02-25766-3153
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Best Local Similarity 58.9
   Sequence 55,
   GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
APPLICANT: ISIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
   PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
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CURRENT APPLICATION NUMBER: US/10/018,407A
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PRIOR FILING DATE: 1999-06-25
  APPLICANT: APPLICANT:
  NUMBER OF SEQ ID NOS: 47
  CURRENT APPLICATION NUMBER: PCT/US02/25766 CURRENT FILING DATE: 2002-08-14
  APPLICANT: YAMAMOTO, Jun

TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
   FEATURE:
  TYPE: DNA
ORGANISM: Homo sapiens
   4348 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccaccccccgctggg 4407
   4408 ggtgggggggggtgtccgtccggaaatgaaggaatagcccgaggacc 4454
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  TYPE: DNA
   4262 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccacccccgctggg 4321
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   3 tecegetgggcaggegggeageteceggegetecteggagaecaetgegetecaegttga 62
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63; Conserv
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   WAGA, Iwao
  SASAI, Hitoshi
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  29.3%;
58.9%;
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58.9%;
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; ORGANISM: Human
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  PCT-US02-23766-55
  Sequence 12, Application US/10137113 GENERAL INFORMATION:
   SOFTWARE: PatentIn version 3.1 SEQ ID NO 55 LENGTH: 10883
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APPLICANT: Kepur, Vivek
APPLICANT: Bannantine, John P.
TITLE OF INVENTION: Mycobacterial Diagnostics
FILE REFERENCE: 09531-112001
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  Matches
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Best Local Similarity 60.2%;
   SOFTWARE: Pa
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  CURRENT APPLICATION NUMBER: US/10/205,951
CURRENT FILING DATE: 2002-07-26
  APPLICANT: Le, Wei-dong
APPLICANT: Vassilatis, Demetrios K
TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
FILE REFERENCE: P02512US1
   NUMBER OF SEQ ID NOS: 124
   PRIOR APPLICATION NUMBER: US 60/308,294 PRIOR FILING DATE: 2001-07-27
   FILE REFERENCE: P02512WO1
CURRENT APPLICATION NUMBER: PCT/US02/23766
CURRENT FILING DATE: 2002-07-26
   APPLICANT: Le, Wei-dong
APPLICANT: Vassilatis, Demetrios K
TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
   CURRENT FILING DATE: 2002-07-26
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PRIOR FILING DATE: 2001-07-27
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  5628 TACTGGCACCAAGGCAGAGGGCACACTCCGAGG 5596
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   5628 TACTGGCACCAAGGCAGAGGGCACACTCCGAGG 5596
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  16 geggggcageteceggegetecteggagaceaetgegetecaegttgaggtggggggtgggg 75
  27.0%;
Local Similarity 60.2%;
les 56; Conserva++...
  76 ggcggacaggaattgaagcggaagtctgggaag 108
   16 gcggggcagctcccggcgctcctcggagaccactgcgctccacgttgaggtgggggtgggg 75
   σ
  56;
   PatentIn version 3.1
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   0; Mismatches
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Pred. No. 14;
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   Score 33.8; DB 1; Length 10883; Pred. No. 14;
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US-09-918-995-29556/c
; Sequence 29556, Application US/09918995
; GENERAL INFORMATION:
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  ; NAME/KEY: misc_feature
; LCCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29556
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   US-10-211-625-47/c
   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1110
                               Sequence 47, Application US/10211625
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PM034C1N
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   Query Match
  SEQ ID NO 29556
  Query Match
Best Local Similarity
  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
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PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRETSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 109
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CURRENT FILING DATE: 2002-04-30
CURRENT APPLICATION NUMBER: US/10/211,625
CURRENT FILING DATE: 2002-08-05
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ORGANISM: Homo sapiens
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  645 GAGACCGGGGTGTTGGCGGGCAAGACACGGCGGCCCTTGGATTCCACGGTGCTCGACGAT 586
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   453 GGTGGGGAAGGTGGAGGCTGGCAGCAGCCCCAGCGCTTGAGTTGGGGGGTCGGCCTCGG 394
   61 gaggtgggcgtggggggc 78
   393 GGACGGGCCTGGGTGAAGGGCAGGCCTGGGA 362
   Local
   75 gggcggacaggaattgaagcggaagtctggga 106
   15 ggcggggcagctccggcgctcctcggagaccactgcgctccacgttgaggtgggcgtggg 74
   1 gatcccgctgggcaggcgggcagctcccgggcgctcctcgggagaccactgcgctccacgtt 60
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59.8%;
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SEQ ID NO 178
LENGTH: 3265
TYPE: DNA
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PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 470
  PRIOR APPLICATION NUMBER: 09/758,468
PRIOR TILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 66/179,065
PRIOR FILING DATE: 2000-01-31
  SOFTWARE: PatentIn Ver. 2.0
   PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: DE 198 13 835.0
PRIOR FILING DATE: 1998-03-20
NUMBER OF SEQ ID NOS: 210
  CURRENT APPLICATION NUMBER: US/09/646,569
CURRENT FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: PCT/DE99/00909
  APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE
FILE REFERENCE: ALBRE 8
  APPLICANT:
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   APPLICANT:
   APPLICANT:
  APPLICANT: SPECHT, THOMAS
   LOCATION: (2012)
OTHER INFORMATION: n equals
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LOCATION: (2113)
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LOCATION: (2109)
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  FEATURE:
  LOCATION:
   NAME/KEY: misc_feature
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  1688 GGTGGGGAAGGTGGAGGGCTGGCAGCCAGCCCCAGCGCTTGAGCTGGGGGTCGGCCTCGG 1629
  15 ggcggggcagctccggcgctcctcggagaccactgcgctccacgttgaggtgggcgtggg 74
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  75 gggcggacaggaattgaagcggaagtctggga 106
   2114
   L Similarity
55; Conserv
  (2066)
   HINZMANN, BERND
SCHMITT, ARMIN
PILARSKY, CHRISTIAN
   DAHL, EDGAR
   Conservative
   26.2%;
   a,t,g, or
   Score 32.8; I
Pred. No. 26;
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  DB 6;
   37;
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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 178
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-569A-178
   ρ
   망
   δÃ
   PCT-US02-18947-329
   δÃ
   밁
   Š
   US-09-646-569A-178
   SEQ ID NO 329
LENGTH: 3656
   GENERAL INFORMATION:
APPLICANT: Rosetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-228
   Sequence 329,
  GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERN
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRI
  Matches
  Query Match
Best Local :
   CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
  TITLE OF INVENTION: HUMBER: US/09/646,569A

CURRENT APPLICATION NUMBER: US/09/646,569A

CURRENT FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: PCT/DE99/0099

PRIOR APPLICATION NUMBER: DE 198 13 835.0

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

NUMBER OF SEQ ID NOS: 210

NUMBER OF SEQ ID NOS: 210

NUMBER OF SEQ ID NOS: 210
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  APPLICANT:
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   180 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 239
   240 ggcagagctcggcccgcggctgaaggggaaaccgcaggagcggcagcggcagtgga 295
   69 cgtggggggggggaagtatgaagcggaagtctgggaagctttagggtcgctgga 124
   180 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 239
   69 cgt9g9g9g9cggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
  Local Similarity
   9 tgggcaggcggggcagctccggcgctcctcggagaccacttgcgctccacgttgaggtggg 68
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  ROSENTHAL,
  HINZMANN, BERND
SCHMITT, ARMIN
PILARSKY, CHRIST
  DAHL, EDGAR
   Application PC/TUS0218947
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  26.2%;
  CHRISTIAN
   26.2%;
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  Score 32.8;
Pred. No. 26;
   Score 32.8;
Pred. No. 26;
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  DB 5;
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  Sequence 1, Application US/10018311A GENERAL INFORMATION:
   APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Pete
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chri
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  APPLICANT: MIYATA, TOShio
APPLICANT: KUROKAWA, Kiyoshi
TITLE OF INVENTION: Meg 3 protein
FILE REFERENCE: 2605/101
  Query Match
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
   TITLE OF INVENTION: Diagnosis and Prognosis FILE REFERENCE: 9301-175-999 CURRENT APPLICATION NUMBER: US/10/172,118 CURRENT FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: 60/380,770 PRIOR FILING DATE: 2002-05-14 NUMBER: OF SEQ ID NOS: 2699
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   601 ggcagagctcggcccgcggctgaaggggaaaccgcaggagcggcagcggcagtgga 656
   541 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 600
   541 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 600
   69 cgtggggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
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  69 cgt9g9g9g9g9gacaggaattgaagcggaagtcttgggaagctttagggtcgctgga 124
   9 tgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttgaggtggg 68
   9 tgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttgaggtggg 68
   64;
   Linsley, Peter
Mao, Mao
Roberts, Chris
  Van 't Veer, Laura
Van de Vijver, Marc
Bernards, Rene
  Application US/10172118
   Conservative
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Pred. No. 25;
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US-09-919-002-3827
   PCT-US02-23766-1/c

: Sequence 1, Application PC/TUS0223766

: GENERAL INFORMATION:
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   US-10-018-311A-1
  Query Match
Best Local 9
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APPLICANT: Le, Wei-dong
APPLICANT: Vassilatis, Demetrios K
TITLE OF INVENTION: Mutant Nurr1 Gene in Parkinson's Disease
FILE REFERENCE: P02512W01
CURRENT APPLICATION NUMBER: PCT/US02/23766
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/308,294
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.1
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  TITLE OF INVENTION: LIBRARIES

FILE REFERENCE: 20411-752CON1

CURRENT APPLICATION NUMBER: US/09/919,002

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922

PRIOR FILING DATE: FILING DATE: 1999-07-22

PRIOR PRIOR ETLING DATE: APPLICATION NUMBER: US 09/034,341

PRIOR FILING DATE: FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 13203
  APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
  APPLICANT: Leshkowitz, Dena APPLICANT: Liu, Jin
  FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: 3395, 3437, and 3440
OTHER INFORMATION: N=G,A,C or T
  ORGANISM: Homo sapiens
   1165 ggacggggcctgggtgaagggcaggcctggga 1196
  1105 ggtggggaaggtggagggctggcagcaggccccagcgcttgagctģggggtcggcctcgg 1164
   763 ggcagagctcggcccgcggctgaaggggaaaccgcaggagcggcagcggcagtgga 818
   703 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctˈgggccctgagctgaa 762
   75 gggcggacaggaattgaagcggaagtctggga 106
   15 ggcggggcagctccggcgctcctcggagaccactgcgctccacgttgaggtgggcgtggg 74
   Local Similarity 59.8
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   9 tgggcaggcggggcagctccggcgctcctcggagaccacttgcgctccacgttgaggtggg 68
  26.2%; Score 32.8; 59.8%; Pred. No. 25;

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   Indels 0; Gaps
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OTHER INFORMATION: n = unknown
   ORGANISM: Human
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   TYPE: DNA
4503 TACTGGCACCAAGGCAGAGGGCACANTCCGAGG 4471
   4563 GCAGGCAGCTTCGGCGGACCCCGGAGAGCTGGGCAGTCCCGGGAGAGCTGGGGCTGGGC 4504
                               76 ggcggacaggaattgaagcggaagtctgggaag 108
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8, 2002, 01:10:21

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

Query

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|-------|-------------------|--------------|--------|-------|--------|-------|---------|-------|--------|-------------------|------------------|-------------------|--------------------|-------------------|------------|---------------------|---------|----------|--------|-------------------|-----------|-------------|-------------------|--------------------|------------|------------|--------------------|----------|-------|-------------|
| 31    | 2 2               | 28           | 27     | 26    | 25     | 24    | 23      | 22    | 21     | 20                | 19               | 18                | 17                 | 16                | 15         | 14                  | 13      | 12       | 11     | 10                | 9         | æ           | 7                 | σ                  | ഗ          | 4          | w                  | N        | _     | NO.         |
| 80 0  | 0 00              | 85           | 9      | 9.    | 89.2   | 9     |         | 95    | 101.8  | 101.8             | •                | 109.4             | 112                | 112.4             | 121.8      | 121.8               | 121.8   | 123.4    |        | 123.4             | 125       | 125         | 125               | 125                | 125        | 125        | 125                | 125      | 125   | Score       |
| 68.0  |                   |              |        |       | 71.4   |       | ۲       | 5     | 81.4   | <u>-</u>          | 7.               | 87.               | 89.                | 89.               | 97.        |                     | 97.4    |          | 98.7   |                   |           | •           | •                 | •                  | •          |            | •                  | 100.0    | 100.0 | Match 1     |
| 371   | 3 5 5             | 355          | 2760   | 2760  | 2760   | 2760  | 2760    | 443   | 362    | 362               | 2165             | 2165              | 495                | 1655              | 404        | 404                 | 404     | 575      | 419    | 419               | 45121     | 3212        | 1732              | 1732               | 1368       | 720        | .324               | 318      | 266   | Length      |
| 3 F   | 1 6               | 18           | 25     | 25    | 25     | 25    | 25      | 19    | 23     | 19                | 31               | 26                | 25                 | 5                 | 34         | 17                  | 17      | 18       | ω<br>5 | 18                | 36        | 32          | 25                | 25                 | 71         | 32         | 17                 | 25       | 32    | DB          |
| 3-143 | -09-431-51/       | -09-431-517- | -09-65 | 9-65  | -09-65 | -65   | -64     |       | 7      | US-09-522-303-847 | US-09-802-669-94 | US-09-665-615B-94 | us-09-652-911-4924 | 2-373-10          | 9-904-013- | US-09-362-510A-3927 | 510-392 | -275-331 | -14    | 9-489-036         | 9-997-722 | -09-834-291 | -09-652           | US-09-644-867-7725 | 24-185-988 | 9-834-291- | US-09-396-087-4122 | -127-278 | _     | ID          |
|       | Sequence 12134, A | 12151        |        | 16/2, | 1930,  | 1000, | e alal, | 1341, | 898, A | Sequence 847, App | 94,              | Sequence 94, Appl | Sequence 4924, Ap  | Sequence 10224, A | 3927,      |                     | 3927,   | `        |        | Sequence 818, App |           | ~           | Sequence 10283, A | Sequence 7725, Ap  | •          |            | 4 L Z              | 2/80     | 32,   | Description |

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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
  US-09-652-127-2780/c
  δõ
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  US-09-834-291-32
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TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
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  Q
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  B
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  89
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   29
  99
   61
```

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; APPLICANT. V----
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY
FILE REFERENCE: MLN98-39PM
CURRENT FILLING DATE: 1999-09-14
CURRENT FILLING DATE: 1999-09-14
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OTHER INFORMATION: Incyte ID No: 1383957.6

NAME/KEY: unsure

LOCATION: 1156, 1235, 1267, 1304, 1364

OTHER INFORMATION: a, t, c, g, or other

US-60-324-185-9888
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   밁
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US-60-324-185-9888/c
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PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
  APPLICANT: Morris, MacDonald APPLICANT: Lal, Preeti APPLICANT: Diep, Dinh
  TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122
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   SOFTWARE: PatentIn Ver. 2.1
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QΥ
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US-09-644-867-7725
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PRIOR FILING DATE: 1999-08-27
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  CURRENT FILING DATE: 2000-08-31 PRIOR APPLICATION NUMBER: 60/152,106 PRIOR FILING DATE: 1999-08-31
   APPLICANT: Holtzman, Douglas A.
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TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1190-001
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CURRENT FILING DATE: 2000-08-31
   APPLICANT: Culpepper, Janice A.
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TITLE OF INVENTION: THEREFOR
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0,

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              SOFTWARE: Pa
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PRIOR ETILING DATE: 2001-03-02
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
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CURRENT FILING DATE: 2001-11-30
  APPLICANT: Morris, David
APPLICANT: Engelhard, E
   TITLE OF INVENTION: p53 Binding Areas FILLE REFERENCE: 4121-122 CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: PCT/DE99/03343 PRIOR FILING DATE: 1999-10-18 PRIOR APPLICATION NUMBER: DE 198 47 779.1
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   APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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CURRENT FILING DATE: 2000-01-19
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SEQ ID NO 818
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 783
                                  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 783
CURRENT APPLICATION NUMBER: US/09/943,143
CURRENT FILING DATE: 2001-08-30
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APPLICANT: HYSEG, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
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FILE REFERENCE: 20411-759CON1
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CURRENT FILING DATE: 1999-07-27
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EARLIER FILING DATE: 1998-12-30
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CURRENT ETLING DATE: 2001-07-12
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PRIOR APPLICATION NUMBER: US 09/221,820
PRIOR APPLICATION NUMBER: US 09/221,820
PRIOR APPLICATION NUMBER: US 09/221,820
PRIOR FILING DATE: 1998-12-30
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DB
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3 US-09-017-706-7

3 US-09-017-706-8

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1 US-08-396-656-2
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| RESULT 2 US-09-428-517-1/c  US-09-428-517-1/c ; Sequence 1, Application US/09428517 ; Patent NO. 6251636 ; GENERAL INFORMATION: APPLICANT: Betlach, Mary C. ; APPLICANT: Shah, Sanjay Krishnakant APPLICANT: Tang, Li ; APPLICANT: Tang, Li ; APPLICANT: Tang, Li ; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE ; FILE REFERENCE: 30062-20029.00 ; CURRENT APPLICATION NUMBER: US/09/428,517 ; CURRENT FILING DATE: 1999-10-28 | Qy       3 tcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttga 62         1 | Query Match 29.3%; Score 36.6; DB 3; Length 4743; Best Local Similarity 58.9%; Prod. No. 0.031; Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps | RESULT 1 US-09-339-964-1 US-09-339-964-1 ; Sequence 1, Application US/09339964 ; Patent No. 6025198 ; GENERAL INFORMATION: APPLICANT: C. Frank Bennett ; APPLICANT: Lex M. Cowsert ; TITLE OF INVENTION. ANTISENSE MODULATION OF SHIP-2 EXPRESSION ; FILE REFERENCE: RTS-0065 ; CURRENT APPLICATION NUMBER: US/09/339,964 ; CURRENT EATING DATE: 1999-06-25 ; NUMBER OF SEQ ID NOS: 47 ; SEQ ID NO 1 ; LENGTH: 4743 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FATURE: ; NAME/KEY: CDS ; LOCATION: (212)(3988) US-09-339-964-1 | ALIGNMENTS | 1 27 21.6 3319 1 US-08-280-845-1 Sequence 1, 27 21.6 3319 2 US-08-428-414A-4 Sequence 4, 27 21.6 3319 5 PCT-US94-00324-2 Sequence 2, 27 21.6 1624 4 US-08-430-225A-19 Sequence 19 26.8 21.4 1624 4 US-08-750-703-2 Sequence 2, 26.8 21.4 1737 2 US-08-750-703-2 | 5 27 21.6 1608 2 US-08-211-718 8 Sequence 8, 27 21.6 2071 4 US-09-816-088-1 Sequence 1, 27 21.6 2362 4 US-09-232-200-48 Sequence 48 27 21.6 2362 4 US-09-232-197-48 Sequence 48 27 21.6 2362 4 US-09-232-197-48 Sequence 48 27 21.6 2362 4 US-09-232-197-48 Sequence 48 27 21.6 2362 4 US-09-232-201-48 Sequence 48 28 28 28 29 29 29 29 29 29 29 29 29 29 29 29 29 | c       28       27.4       21.9       921       1       US-08-396-650-3       Sequence 3, App         c       29       27.4       21.9       921       1       US-08-396-650-4       Sequence 4, App         c       30       27.4       21.9       921       1       US-08-768-626-3       Sequence 3, App         c       31       27.4       21.9       921       1       US-08-768-626-4       Sequence 4, App         c       32       27.4       21.9       921       1       US-08-984-709A-52       Sequence 52, App         c       32       27.4       21.9       1413       4       US-08-984-709A-52       Sequence 2, App         33       27.2       21.8       4157       2       US-08-162-146-2       Sequence 2, App         34       27.2       21.8       4157       2       US-08-136-146-2       Sequence 2, App |  |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 07                                                                                   | _                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | ppi<br>ido<br>ido<br>ido<br>ido<br>ido<br>ido<br>ido<br>ido<br>ido<br>id                                                                                                                                                                                        | ppli<br>ppli<br>ppli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |  |

EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16

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  APPLICANT: Kaser, Matthew, R.
APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: LIPID METABOLISM TRANSCRIPTION FACTOR
FILE REFERENCE: PC-0004 US
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EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
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LOCATION: 186, 189, 195, 196, 200, 204, 208, 2
NAME/KEY: unsure
LOCATION: 228, 236, 244, 248, 251
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TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
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COUNTRY: Canada

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APPLICANT: Owolabi, Joshua
APPLICANT: Rampersad, Vikarna
APPLICANT: Kamboj, Rajender
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  APPLICANT: Kamboj, Rajender
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6850 Goreway Drive
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CURRENT APPLICATION DATA:
             TELECOMMUNICATION INFORMATION:
   APPLICATION NUMBER: US/0 FILING DATE: 19920810 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
   APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: A No. 5569601el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
   CORRESPONDENCE ADDRESS:
   REFERENCE/DOCKET NUMBER: AL TELECOMMUNICATION INFORMATION: TELEPHONE: (416)-868-1482
   PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/CA94/00538

FILING DATE: 27-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: RIDOUT & MAYBEE, Attn. Robert G. Hirons
  SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
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   Chicago
: Illinois
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  Application US/07928611
   E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
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TITLE OF INVENTION: A NO. 6203998el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6203998nan, Kevin E
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Mismatches

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; Patent No. 5516683
  ₽
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   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/056,051
FILING DATE: 1930429
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5516683nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEFAX: 312-715-1234
   Matches
  Query Match
Best Local Similarity
   TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 5:
   GENERAL INFORMATION:
   ALL.
STREET: LU
CITY: Chicago
CITY: Illinois
TWATE: IISA
                                   1062 CCCCGGGAAGGCCGGGGGGGGGGGGCGCACAGTCGGGGCCCCAGGGGTCCTGGGGGAGG 1003
   FEATURE:
  SEQUENCE CHARACTERISTICS:
   CORRESPONDENCE ADDRESS:
   APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.-M.
TITLE OF INVENTION: A NO. 5516683el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 6
   FEATURE:
   APPLICANT:
APPLICANT:
   MOLECULE TYPE: cDNA
   561 CCCCGGGGAAGGCCGGGGGGGGGGGGCCGCACAGTCGGGGGGCCGCAGGGGTCCTGGGGGAGG 502
  501 CCGGGCGCGGGGCGCACAGTCGGGGCCGCAGGGGTCCGGG 460
65 -tgggcgtggggggggacaggaattgaagcggaagtctggg 105
   LOCATION:
  LENGTH: 1610 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
  65 -tgggcgtggggggggacaggaattgaagcggaagtctggg 105
  NAME/KEY:
   LOCATION:
   NAME/KEY:
  TOPOLOGY:
   5 ccgctgggcaggcgggcagctcctgggagaccactgcggtccacgttgagg 64
   ADDRESSEE:
   σ
   62;
  60606
   E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
  Conservative
  Grandy, David K
Bunzow, James R
   5'UTR
1..103
  linear
   3'UTR
1508..1610
  104..1507
  22.1%;
  ; Score 27.6; DB 1;
; Pred. No. 11;
0; Mismatches 39;
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  Indels
  1;
  Gaps
  1;
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Db 1002 CCGGGGGGGGGGCGCACAGTCGGGGCCGCAGGGGTCCGGG 961

Search completed: September 7, 2002, 18:23:12 Job time: 28886 sec

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Title:
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  Result
No.
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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  Scoring table:
  Run on:
   OM nucleic - nucleic search, using sw model
   Database
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  125
36.6
32.8
32.8
32.4
32.4
32.2
32.3
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  266
4743
3768
3995
1110
1110
1388
511
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22
22
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23
21
22
22
   ij
AAZ88700
AAZ91408
AAC81955
AAI68201
AAS29777
AAL01443
AAC44059
AAK92251
AAK923511
  SUMMARIES
   Compugen Ltd.
   3472872
                     Human cytoskeletal
Human reproductive
Zea mays DNA fragm .
Human cDNA 5'-end
  Description
  Human Meg-3 cDNA.
Human osteoclast e
   Human CD95 recepto
Human Ship-2 nucle
  Human cDNA clone
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| /BQO138480/BQO13848                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                       |
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| ○ 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 0.0.0 J. 1. 1. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.                                                                                                                                                                                                                                                                                                 |
| 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | n in in a p in                                                                                                                                                                                                                                                                                                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                       |
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| ABL19753 AAK91993 AAK91993 AAK93732 AAF94082 AAF94082 AAS76156 AAS76184 AAK94348 AAF93879 ABL19752 AAD05562 AAD05562 AAD055613 AAK73537 ABBA16261 AAS79912 AAS8577912 AAS855776 AAS89212                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AAS29822<br>AAL05199<br>AAK94547<br>AAV43618<br>AAQ87721<br>AAQ87722<br>AAT28387<br>AAT28388<br>AAT17409<br>AAF76957<br>AAF76957<br>AAF76957<br>AAF76952<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962<br>AAF76962                      |
| phila meland cDNA clone r specific f end coding nove full-length cDNA encoding nove full-length cDNA encoding secreted proper specific from ays DNA fracecreted proper secreted proper secrete | Human cytoskeletal Human reproductive Human full-length Human secreted pro Human auxillary cy Human auxillary cy Human cytochrome p Human cytochrome p Human derived cyto Human derived cyto Human derived cyto Human liver cell s Genetic construct DNA encoding novel 1 2.301 kb SM-MHC-pr Human secreted pro Streptomyces venez HSV-2 strain SB5 C |

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## ALIGNMENTS

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ARESULT

AAZ88770

AAZ8877

AAZ AAZ8

AC AAZ8

A
   p53; CD95 receptor; human; screening; apoptosis-modulation; cancer chemotherapy; ss.
   Human CD95 receptor intron 1 fragment.
  11-MAY-2000 (first entry)
   AAZ88700;
   AAZ88700 standard; DNA; 266 BP
   Krammer P, Mueller-Schilling M, Oren M;
  16-OCT-1998;
   03-FEB-2000.
  DE19847779-C1.
   protein_bind
   Homo
   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
   16-OCT-1998;
   sapiens.
   98DE-1047779
   98DE-1047779
   Location/Qualifiers 160..179
   /bound_moiety= p53
  /*tag=
```

```
ACX ACX DESCRIPTION OF STATE O
  RESULT
AAZ91408
   Š
  В
  SXX CCC CCC CCC XXX PT XXX
   QУ
   В
  Ωy
   Matches
  Query Match
Best Local
Example 13; Column 41-52; 34pp; English
  Antisense oligonucleotides, useful for inhibiting human Ship-2 expression and for detecting nucleic acids encoding Ship-2 -
  WPI; 2000-181819/16.
P-PSDB; AAY80120.
  Bennett CF,
  25-JUN-1999;
   25-JUN-1999;
  15-FEB-2000.
   US6025198-A.
   Human; Ship-2; antisense oligonucleotide; phosphorothioate; detection; inhibition; SH2-containing phosphatidylinositol phosphatase-2; ss.
  (ISIS-) ISIS PHARM INC.
   Homo sapiens
  Human Ship-2 nucleotide sequence SEQ ID NO:1.
   22-MAY-2000
  This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apontosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 bin region described in the method of the invention.
   AAZ91408;
   AAZ91408 standard; cDNA; 4743 BP
   Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy \, -
  Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
  121
  WPI; 2000-162245/15.
   121 tggag 125
  61
   61
   Local Similarity
  \vdash
  1 gatcccgctgggcaggcggggcagctcctcggcgctcctcggagaccactgcgctccacgtt 60
   ν
   tggag
   gaggtgggcgtggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
  gatcccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgtt 60
  9a9gt9g9cgt9g9g9gcggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
  125;
   2; Fig 4; 12pp; German.
  125
  Cowsert
  (first entry)
   Conservative
   99US-0339964
  99US-0339964.
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  /product= "Ship-2"
  /*tag=
  Ĭ,
   100.0%;
   0,
  Score 125; DB 21;
Pred. No. 2.2e-26;
  Length 266;
   Indels
   0,
   resents a
p53 binding
  Gaps
  0;
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DR DR DR PT PT CCC CCC CCC
  PA
  YR XX
  PD
XX
PF
   RESULT
AAC81955
  В
   QΥ
  В
  ΩV
   Query Match
Best Local S
   Matches
   {\tt Meg-3} protein expressed in mesangial kidney cells for diagnosis treatment of kidney disease -
   Claim 4; Page 44-53; 65pp; Japanese.
  P-PSDB; AAB11456.
  WPI; 2000-687536/67.
  Miyata T;
   Meg-3; human; mesangial kidney cell; treatment; diagnosis; antidiabetic; vaccine; gene therapy; pathogenesis; kidney ciglomerulonephritis; diabetes; proliferation; ss.
   The present invention describes phosphorothioate antisense oligonucleotides that specifically hybridise with, and inhibit the expression of, nucleic acids encoding human Ship-2 (also called SH2-containing phosphatidylinositol phosphatase-2). Also described is a method of inhibiting the expression of Ship-2 in human cells or tissues in vitro comprising contacting the cells with the phosphorothicate antisense oligonucleotides. The phosphorothicate
   (MIYA/) MIYATA T.
  30-APR-1999;
   28-APR-2000; 2000WO-JP02831.
   WO200066729-A1
  Homo sapiens
  Meg-3; human;
   AAC81955 standard; cDNA; 3768 BP
  4408 ggtgggggggggtgtccgtccggaaatgaaggaatagcccgaggacc 4454
   4348 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccacccccgctggg 4407
  antisense oligonucleotides can be used to treat animals (especially humans) suspected of having or being prone to a disease or condition associated with Ship-2 expression. The present sequence encodes
   (KURO/) KUROKAWA K.
  Human Meg-3 cDNA
  01-MAR-2001
  AAC81955;
   Sequence 4743 BP; 939 A; 1466 C; 1448 G; 890 T; 0 other;
  human Ship-2.
  63 ggtgggcgtggggggggaaggaattgaagcggaagtctgggaagc 109
  3 tecegetgggeaggegggeageteetgggegeteeteggagaceaetgegeteeaegttga 62
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  (first entry)
  99ЛР-0123561
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  2
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  Score 36.6;
  Pred
  Mismatches . 44;
  . No. 0.31;
  DB 21;
  Indels
  Length
   kidney disease;
  condition
  0,
   Gaps
  0
```

This invention describes a novel protein highly expressed in mesa kidney cells which has renal and antidiabetic activity and which

mesangial

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  Matches
  Query Match
Best Local (
                                    Matches
  used in a vaccine or for gene therapy. The proteins and nucleic acids may be used for the investigation of the function of the Meg-3 protein and its role in the pathogenesis of kidney disease and for the treatment, prevention and diagnosis of kidney disease in which mesangial cell proliferation is implicated, such as glomerulonephritis and diabetes.
  Sequence 3768 BP; 722 A; 1136 C; 1190 G; 717 T; 3 other;
   JP2001231573-A
   Human; osteoclast;
   Human
   AAI68201;
  AA168201 standard; cDNA; 3995
  The invention relates to human osteoclast expressed polynucleotide sequences (AAI68200-AAI68203) and the encoded proteins (AAM51208-AAM51211). The polynucleotides are useful as an index formaturation of osteoclasts.
   21-FEB-2000; 2000JP-0048886
   21-FEB-2000; 2000JP-0048886
   28-AUG-2001.
  18-DEC-2001 (first entry)
   Sequence 3995 BP;
   Claim 1; Page 14-18; 31pp; Japanese.
   (SHIO ) SHIONOGI & CO LTD
  763 ggcagagctcggcccgcggctgaaggggaaaccgcaggagcggcagcggcagtgga 818
  703 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 762
  69
  9
            9
   osteoclasts
  tgggcaggcggggcagctccggcgctcctcggagaccactgcgcctccacgttgaggtggg 68
   cgtggggggcggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
tgggcaggcggggcagctcctgggagaccactgcgctccacgttgaggtggg
   2001-609964/70.
  sapiens.
  derived from human osteoclast, used as
  osteoclast expressed
  64;
  Similarity
   Similarity
  AAM51209
   Conservative
                                    Conservative
   Location/Qualifiers 235..2475
  /*tag= a
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   755 A; 1222 C; 1308 G; 710 T; 0 other;
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Pred. No. 3
  Score 32.8;
Pred. No. 3
   ВÞ
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                                       Mismatches
  .6;
   6,
   DB
  DΒ
  52;
  an index for
  21;
                                    52;
   IJ
  protein"
   NO.
                                    Indels
   Length
  Indels
  Length
   an index for the
  the maturation
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                                      0;
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                                       Gaps
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  1777/c
AAS29777 standard; cDNA;
   Cytoskeletal element-related protein; human; mouse; rabbit; goat;
   AAS29777;
  31-JAN-2000;
  02-AUG-2001.
  WO200155168-A1
   tissue
   Human cytoskeletal element-related polypeptide encoding cDNA #8
   21-NOV-2001 (first entry)
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  11-JUL-2000;
14-JUL-2000;
  30-JUN-2000;
07-JUL-2000;
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  17-JAN-2001;
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   984
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  18-APR-2000;
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   cgtggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
  regeneration; anti-infertility; food additive.
2000US-0225759
2000US-0226279
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2000US-0225447.
  2001WO-US01331
  2000US-0198123.
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  1110
  ВP
   983
   horse;
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QΥ
  밁
   Qy
  Sequences AAS29770-AAS29813 represent cDNA molecules, which encode the Cytoskeletal element-related polypeptides of the invention. Cytoskeletal Cytoskeletal element-related polypunclectides are useful in the Cytoskeletal polypeptides and their associated polynuclectides are useful in the Cytoskeletal polypeptides and their associated polynuclectides are useful in the Cytoskeletal polynucleotide. The treatment and prevention of various types of disorders in e.g. Cytoskeletal polynucleotide. The treatment of a mutation in a cytoskeletal polynucleotide. The treatable Cytoskeletal polynucleotide. The treatable Cytoskeletal polynucleotide of the presence or absence of a mutation in a cytoskeletal polynucleotide. The treatable Cytoskeletal polynucleotide. The treatable Cytoskeletal polynucleotide. The treatable Cytoskeletal polynucleotide. The treatable Cytoskeletal polynucleotide. The breast or liver, Cytoskeletal polynucleotides are set breast or liver, Cytoskeletal polynucleotides are
   Query Match
Best Local S
Matches 66
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05-DEC-2000;
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06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
   Claim 1; SEQ ID No 18; 505pp; English.
  Novel isolated human cytoskeletal element-related polypeptide useful for diagnosis/treatment of neoplastic disorders, disorders associated with neural transmission, chromosomal abnormalities, autoimmune
  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
  Note:
  WPI; 2001-476182/51.
P-PSDB; AAU18515.
   Rosen CA,
  716
  (HUMA-) HUMAN GENOME SCI INC
63 ggtgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctg 122
   ω
   tcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttga 62
   TGCCGCTGGCCAGGAGCTGCATGAGGAGCTCCGTGATGTCCCTGCCCGCCACGTGGA
   The sequence
   66; Conserv
   Barash SC,
   Conservative
   2000US-0251868.
2000US-0251869.
2000US-0251989.
  2000US-0249212.
2000US-0249213.
2000US-0249214.
2000US-0249215.
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3-0246611. 3-0246613.

Gaps

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2000US-0246609 2000US-0246610

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|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|------------|----------------|------------------------------------------|------------------|
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |       |            |                |                                          |                  |
| אים<br>ארק את המקר המקר המקר המקר המקר המקר המקר המקר                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PR    | PR<br>PR   | PR             | PR                                       | P R              |
| 14 - SEP - 2000 21 - SEP - 2000 21 - SEP - 2000 25 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000 20 - CCT - 2000 02 - CCT - 2000 02 - CCT - 2000 02 - CCT - 2000 03 - CCT - 2000 04 - CCT - 2000 05 - CCT - 2000 07 - CCT - 2000 08 - NOV - 2000 09 - NOV - 2000 01 - NOV - 2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 000   | 000;       | 000;           | 00;                                      | 00;              |
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AC AAC440
XX Zea ma
XX Zea ma
KW Hybrid
KW Protei
KW Pathwa
XX Zea ma
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  밁
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   δÃ
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   Query Match
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   Sequence 1110
   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
   WPI; 2001-465570/50.
P-PSDB; AAM95473.
  Claim
  Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
  596
   (HUMA-) HUMAN GENOME SCI INC
   123
   656
  716
  63
  ω
  CA 595
   ga 124
   tcccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgttga 62
  GCTTGGTGACTGCGTGGGGCAGGGAGTAACCCTCAAAGATGGGGACAGTGCAGGTGACCG
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99US-0144085

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CS Homo sapiens.
XX
OS Homo sapiens.
XX
PD 05-SEP-2001.
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   Human cDNA 5'-end sequence, SEQ ID
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20-AUG-1999
20-AUG-1999
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11-AUG-1999

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RESULT 9
AAK93511/c
ID AAK935
밁
   Ş
   Db
  QY
  Query Match
Best Local
  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of fill length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
  08-JUL-1999;
11-JAN-2000;
  Homo sapiens
   Human; full length cDNA; cDNA synthesis; oligo-capping; ss
   Human cDNA clone representative sequence, SEQ ID NO: 1971.
   AAK93511;
   AAK93511 standard; cDNA; 511
  08-JUL-1999; 99JP-0194486
11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
            (HELI-) HELIX RES INST
  07-JUL-2000;
  05-SEP-2001
   EP1130094-A2
  06-NOV-2001
   Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;
  Claim
  WPI; 2001-524255/58.
  Ota T,
   Wakamatsu A,
   07-JUL-2000; 2000EP-0114089
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  249 AGGTGGGCAGCGGGGCAGCGCGTGGCCAGACCGCGGGGCAGGAGGG
   309 CCGCGGGGCAGACGCGGCAACAGCGCGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC 250
   65 tgggcgtgggggggggaggaattgaagcggaagtctggggaagctttaggg 116
   госат
  σ
  Primers useful for synthesizing full length cDNA clones and
  ccgctgggcaggcggctccggcgctcctcggagaccactgcgctccacgttgagg
   genetic manipulation
   Similarity
  Nishikawa T,
  SEQ ID NO 711; 1380pp + sequence listing; English
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                                       99JP-0194486.
2000JP-0118774.
2000JP-0183765.
  2000EP-0114089
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  99JP-0194486.
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a T, Nagai
   0;
   Score 32; DB Pred. No. 4.7;
  Mismatches
   Hayashi K,
K, Kojima
   22;
   'n
  50;
  Ishii S, Kawai Y;
S, Otsuki T, Koga
  Length 511;
  Indels
  198
  0;
  Gaps
   Ή,
   64
  0;
```

```
В
  В
  20
  QΥ
  Matches
   Query Match
Best Local :
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
  cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cencerial; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; sastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
  17-JAN-2001; 2001WO-US01331.
   clones. 830 CDNA molecules encoding a human protein have been soluted and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
  WO200155168-A1
  Homo sapiens.
   Cytoskeletal element-related protein; human; mouse; rabbit;
  Human cytoskeletal element-related polypeptide encoding genomic DNA #9.
  21-NOV-2001 (first entry)
  AAS29822 standard; DNA; 1371 BP.
  Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;
   Ota T,
   The invention
  Example 11; SEQ ID NO 1971; 1380pp + sequence listing; English.
  WPI; 2001-524255/58
  Wakamatsu A,
  249
  309 CCGCGGGGCAGACGCGGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC 250
   65 tgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttaggg 116
  Local Similarity 55.0 les 62; Conservative
  5
   Primers useful for synthesizing in genetic manipulation -
  AGGTGGGCAGCGGGGCAGCCGTGGGCTGGCAGACCGCGGGGCAGGAGGG
   ccgctgggcaggcggggcagctccgggagaccactgcgctccacgttgagg 64
   Nishikawa T,
2000US-0179065.
2000US-0180628.
2000US-0184664.
   relates to primers for synthesising full length cDNA
  Sugiyama
   25.6%;
55.4%;
  Isogai T, Hayashi K, I:
na T, Nagai K, Kojima S,
  0;
   Score 32; DB
Pred. No. 4.7;
  Mismatches
  full length cDNA clones and their
  DB 22; Length 511;
  50; Indels
   Ishii S,
  hii S, Kawai Y;
Otsuki T, Koga
  Koga H;
   goat; horse;
  0;
```

0

07-JUN-2000 28-JUN-2000 30-JUN-2000 07-JUL-2000 07-JUL-2000 11-JUL-2000 11-JUL-2000 14-JUL-2000 26-JUL-2000

18-APR-2000; 19-MAY-2000; 2-MAR-2000; 6-MAR-2000; 7-MAR-2000;

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13-OCT-2000
13-OCT-2000
20-OCT-2000
20-NOV-2000
20-NOV-2000
20-OCT-2000
20-NOV-2000
20-NOV
  17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
   17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
  Claim
   disorders
  Novel isolated human cytoskeletal element-related polypeptide useful for diagnosis/treatment of neoplastic disorders, disorders associated with neural transmission, chromosomal abnormalities, autoimmune
   (HUMA-)
  2001-476182/51.
۲,
  CA,
  HUMAN
SEQ
  Barash
  2000US -0237040
2000US -0239935
2000US -0239935
2000US -0241966
2000US -0241786
2000US -0241787
2000US -0241809
2000US -024181809
2000US -0246477
2000US -0246477
2000US -0246477
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2000US -0246477
2000US -0246477
2000US -0246528
2000US -0246528
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2000US -0246528
2000US -0246610
2000US -0246610
2000US -0246611
2000US -0246611
2000US -0249217
2000US -0249217
2000US -0249211
2000US -0249
IJ
  GENOME
No 107;
  sc,
  SCI
  Ruben
505pp; English.
  SM;
   associated
```

2000US-0186350 2000US-019874 2000US-019874 2000US-0215135 2000US-0216867 2000US-0216867 2000US-0217486 2000US-0217487 2000US-0217487 2000US-0218296 2000US-0225266 2000US-0225266 2000US-0225266 2000US-0225266 2000US-0225266 2000US-0225275 2000US-0225277 2000US-0

30-AUG-2000; 01-SEP-2000; 01-SEP-2000;

14 - AUG - 2000; 14 - AUG - 2000; 18 - AUG - 2000; 22 - AUG - 2000; 22 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 23 - AUG - 2000;

26-JUL-2000 14-AUG-2000 
01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 014-SEP-2000 14-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000

```
AALO5199/

ID AALO

XX AALO

XX 21-N

XX Huma

XX Huma

XX Homo

X
  CC in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or caseepe. A pathological condition can be determined by determining the presence or absence of a mutation in a cytoskeletal polynucleotide. The CC treatable disorders include autoimmune diseases such as rheumatoid CC arthritis, hyperproliferative disorders such as neoplasms of the breast CC or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, crivases and fungi, ocular disorders such as corneal infection, endocrine CC disorders such as Premature labour and infertility, gastrointestinal CC disorders such as Crohn's disease, renal disorders such as asthma. The CC disorders such as Crohn's disease, renal disorders such as asthma. The CC due to sumburn, to maintain organs before transplantation, to regenerate CC tissues and in chemotaxis. The polypeptides can also be used as a food cadditive or preservative to increase or decrease storage capabilities.

CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO
  Query Match
Best Local S
Matches 65
  04 - FEB - 2000

24 - FEB - 2000

02 - MAR - 2000

16 - MAR - 2000

17 - MAR - 2000

18 - APR - 2000

19 - MAY - 2000

07 - JUN - 2000

30 - JUN - 2000
  Sequences AAS29814-AAS29838 represent genomic DNA molecules, which encode the cytoskeletal element-related polypeptides of the invention. Cytoskeletal polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders
  02-AUG-2001
  Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; {\tt ds}.
  AAL05199;
   AAL05199 standard; DNA; 1371
   31-JAN-2000;
   17-JAN-2001; 2001WO-US01339
  WO200155320-A2
  Homo
   Human reproductive system related antigen DNA SEQ ID NO: 7887.
   21-NOV-2001 (first entry)
  676
  616
   65
  σ
   ttggtgactgcgtggggcagggagtaaccctcaaagatggggacagtgcaggtgaccgca
   65;
   h 25.6%;
Similarity 54.2%;
                      2000US-0180628.
2000US-018464.
2000US-0186350.
2000US-0189874.
2000US-0199872.
2000US-0299467.
2000US-0299467.
2000US-0214886.
2000US-0215135.
2000US-0216880.
2000US-0216880.
   Conservative
   2000US-0179065
   0;
  Score 32; DB 22; Length 1371; Pred. No. 5.4; 0; Mismatches 55; Indels
  ΒP
   0;
   Gaps
  675
   0,
    33-AUG-2000

30-AUG-2000

31-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

12-SEP-2000

14-SEP-2000

11-SEP-2000

11-CCT-2000

   14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
   14-AUG-2000;
14-AUG-2000;
2000US-0239935
2000US-0249937
2000US-0249960
2000US-0241221
2000US-0241785
2000US-0241787
2000US-0241787
2000US-0241808
2000US-0241808
2000US-0241806
2000US-0241826
2000US-0241826
2000US-0241826
   2000US - 0236368
2000US - 0236369
2000US - 0236370
2000US - 0236802
2000US - 0237037
2000US - 0237037
2000US - 0237038
2000US - 0237038
2000US - 0237034
  2000US-0233065.
2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
   2000US-0220964
2000US-0224518
2000US-0224513
2000US-0225267
2000US-0225267
2000US-0225267
2000US-0225757
2000US-0225757
2000US-0225757
2000US-0225759
2000US-0225759
2000US-0225718
2000US-0226668
2000US-0227182
2000US-0227182
2000US-0229287
2000US-0229287
2000US-0229344
2000US-0231414
2000US-0231414
2000US-0231414
2000US-0231414
2000US-0231468
2000US-0233299
   2000US-0235484.
2000US-0235834.
2000US-0235836.
2000US-0236327.
  2000US-0236367
   2000US-0233064
   2000US-0218290
2000US-0220963
```

δÃ 밁

Qy 밁 Ωy

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```
Best Local
                     Query Match
  Matches
   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention.
   08-NOV-2000;
   08-NOV-2000;
  17-NOV-2000;
  08-NOV-2000;
17-NOV-2000;
  08-NOV-2000
  08-NOV-2000;
   Disclosure; SEQ ID NO 7887; 1297pp + Sequence Listing;
  17-NOV-2000;
  17-NOV-2000;
17-NOV-2000;
  17-NOV-2000;
   17-NOV-2000;
   Sequence 1371 BP; 267 A; 406 C; 430 G;
   17-NOV-2000;
  17-NOV-2000;
   17 - NOV -
  17-NOV-2000;
  17-NOV-2000;
  17-NOV-2000;
   17-NOV-2000;
  Isolated nucleic acid molecule encoding a reproductive system antigen
   17 - NOV -
  17-NOV-2000
  17-NOV-2000
  -NOV-2000;
  -NOV-2000
   -NOV-2000
   2001-465570/50
  65;
            Similarity
  in preventing, treating or ameliorating a medical condition
   HUMAN GENOME
  Barash SC,
  2000US-0246523
2000US-0246526
2000US-0246526
2000US-0246526
2000US-0246527
2000US-0246532
2000US-0246632
2000US-0246611
2000US-0246611
2000US-0246613
2000US-0246613
2000US-0249207
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2000US-0249207
2000US-0249210
2000US-0249211
2000US-0249211
2000US-0249211
   2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
  2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249295.
2000US-0249299.
2000US-0249299.
2000US-0249300.
2000US-0250160.
  2000US-0249213
2000US-0249214
2000US-0249215
2000US-0249215
2000US-0249217
2000US-0249218
2000US-0249218
  Conservative
   2000US-0251856.
2000US-0251868.
2000US-0251869.
   2000US-0246478.
           25.6%;
54.2%;
  0;
           Score 32; DB:
Pred. No. 5.4;
   SM:
  Mismatches
  268 T; 0 other;
                      DB 22;
 55;
                     Length 1371;
  Indels
  English
  0,
   of a
be used
Gaps
  0;
```

```
RESULT 12
AAK94547/c
   Matches
  Query Match
Best Local Similarity
  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
  830\ \mathrm{Primers} useful for synthesizing full length cDNA clones and their use in genetic manipulation -
   08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765
   AAK94547
   Claim
  Ota T,
   07-JUL-2000; 2000EP-0114089
   AAK94547;
  Sequence 1544 BP; 332 A; 381 C; 471 G; 360 T; 0 other;
   WPI;
   Wakamatsu A,
  05-SEP-2001
   Human; full length cDNA; cDNA synthesis; oligo-capping;
  Human full-length cDNA, SEQ ID NO: 3439.
  P-PSDB; AAM93614
   (HELI-) HELIX RES INST
   696
   756
  309
  65
  G
  σ
  tgggcgtgggggggggaagtagaagcggaagtctggggaagctttagggtcgctgga
   CCGCTGGCCAGGAGCAGCTGCATGAGGAGCTCCGTGATGTCCCTGCCCGCCACGTGGAGC
                            ccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttgagg
   TTGGTGACTGCGTGGGGCAGGGAGTAACCCTCAAAGATGGGGACAGTGCAGGTGACCGCA
   ccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttgagg
CCGCGGGGCAGACGCGGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC 250
   2001-524255/58.
   8; SEQ ID NO 3439; 1380pp + sequence listing; English.
   62;
  Nishikawa T,
   standard;
   Conservative
   (first entry)
   Sugiyama
  25.6%;
   Isogai T, Hayashi K, I:
1 T, Nagai K, Kojima S,
   1544
   0;
  Score 32; DB Pred. No. 5.4;
   Mismatches
  22;
   Ishii S, Kav
3, Otsuki T,
   Length 1544;
  Indels
  Kawai
  0
   Gaps
  Η;
   637
   697
  64
```

밁 QΥ DЬ δÃ

249

AGGTGGGCAGCGGGGCAGCGCGTGGGCTGGCAGACCGCGGGGCAGGAGGG tgggcgtggggggggacaggaattgaagcggaagtctgggaagctttaggg 116

0;

65

RESULT 13
AAV43618/c
ID AAV436

AAV43618 standard; DNA; 1553 BP

QУ 밁

Вb

0,

```
CC biological activities, such as cytokine, cell proliferation, or cellular cdifferentiation activities, tissue growth or regeneration, activin or cellular cdifferentiation activity, receptor/ligand activity, haemostatic or cc inhibin activity, receptor/ligand activity, haemostatic or cc anti-inflammatory activity. The proteins can also be used as comparison, or disease-specific alteration in protein expression. They cc an be used in protein interaction assays, to identify ligands or binding cc proteins. Compounds which affect the biological activities of the proteins or their ability to interact with specific ligands can be identified using the proteins in screening assays. The proteins and contibodies that bind specifically to the protein can also be used to design diagnostic tests and therapeutic compositions for diseases which affect be proteins comprising, e.g. signal sequences or transmembrane domains of the proteins can be used to target other protein domains to cellular of the protein can be used to target other protein domains to cellular of the protein can be secreted extracellularly.
Query Match
Best Local Similarity
   This DNA encodes a human secreted protein. The specification provides secreted protein sequences (AAW63691 to AAW63699) encoded by the nucleic acid sequences shown in AAV43611 to AAV43619. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine
   Secreted human polypeptides - having cytokine, cell proliferation differentiation, activin or inhibin, tumour inhibition or
  CDS
   Sequence 1553 BP; 348 A; 384 C; 467
   Claim 6; Pages 45-46; 78pp; English.
  anti-inflammatory activities
   Escobedo J,
   Secreted protein; human; cell proliferation; cytokine activity; tissue growth; cellular differentiation; regeneration; activin; inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; biomarker; ss.
  (CHIR ) CHIRON CORP.
  11-DEC-1996;
   11-DEC-1997;
   WO9825959-A2
  AAV43618
  18-JUN-1998
  HOMO
   24-SEP-1998
  1998-348453/30.
  secreted
   García P,
   (first entry)
   protein 18 encoding DNA.
   96US-0032757.
   97WO-US22787.
  /*tag=
   Location/Qualifiers 65..1495
  /product= "human secreted protein"
 25.6%;
   Hu
   Ó
 Score 32;
Pred. No.
   Kothakota
   <u>ი</u>
 DB
5.4;
   354 T; 0 other;
   ß
                19;
   Williams
                Length 1553;
   or
```

Query Match Best Local Similarity

25.3%;

Score 31.6; Pred. No. 7;

DB

16; Length 1485;

Sequence 1485 BP; 327 A; 430 C; 413 G; 315 T; 0 other

```
AAQ87721
ID AAQ8
  RESULT 14
  Matches
auxiliary cytochrome P450 species 2A6. The gene encodes a protein of 494 amino acids. The cDNA was amplified by PCR using the primers AAQ87751-4. The product was cloned into the yeast expression vectors pAAH5N or pAHRR to produce the vectors p2A6 for the expression vectors pAHFN or pAHRR to produce the vectors p2A6 for the expression vectors path of the cytochrome P450 alone or p2A6R for co-expression with the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 (AAQ87715), 2E1 (AAQ87715) or 3A4 (AAQ87717) or their auxiliary species and variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the
  The nucleotide sequence of the cDNA coding region for the human
  Examples; Page 49-51; 124pp; English.
  expressing human cytochrome p450 and a yeast NADPH-P450 reductase
  Evaluation of safety of a chemical cpd. - using recombinant yeast
   P-PSDB; AAR72367.
   WPI; 1995-116991/16.
   Hayashi K,
Yabusaki Y;
  30-JUL-1993;
  21-JUL-1993;
20-JUL-1993;
  EP644267-A.
   carcinogen; mutagen; liver metabolism; ds.
  Human cytochrome P450; amplification; PCR; primer; expression vector; yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
   Human auxillary cytochrome P450 species 2A6 coding region.
   14-NOV-1995
   AAQ87721 standard; cDNA; 1485 BP
   (SUMO ) SUMITOMO CHEM CO LTD
  (HAYA/) HAYASHI K.
  20-JUL-1994;
  22-MAR-1995
  227 AGGTGGGCAGCGGGGCAGCGCGTGGGCTGGCAGACCGGGGGGCAGGAGGG
   287
  65
  σ
   tgggcgtgggggggacaggaattgaagcggaagtctgggaagctttaggg 116
   ccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttgagg 64
  CCGCGGGGCAGACGCGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC 228
  62;
   Kaneko H,
  Conservative
  (first entry)
   93JP-0180246.
93JP-0201120.
93JP-0208279.
  94EP-0111298
   Komai K,
  0;
  Mismatches
  Nakatsuka I,
  50;
   Sakaki T;
  Indels
  0;
   Gaps
```

```
The nucleotide sequence of the cDNA coding region for the human cauxillary cytochrome P450 species 2A6 variant 1. The gene contains a cc change at base 1427 from A to C as compared to the wild type sequence CC (AAQ87721). This changes the amino acid residue from Arg to Lys. The cDNA CC was amplified by PCR using the primers AAQ87751-4. The product was CC cloned into the yeast expression vectors pAAH5N or pAHRR to product was CC vectors p2A6 variant 1 for co-expression of the cytochrome P450 alone CC or p2A6R variant 1 for co-expression with the yeast NADPH-P450 CC a chemical compound by reacting the chemical compound with recombinantly CC produced human cytochrome P450 molecular species 122 (AAQ87714), 2C9 (CAAQ87715), 2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxillary species and variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a cfused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for CC determining whether the chemical compound, or its metabolite, will be
   Š
  RESULT 15
AAQ87722
  밁
   밁
  Matches
   Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-_{
m l}P450 reductase
  WPI; 1995-116991/16.
  EP644267-A.
  Examples; Page 53-55; 124pp; English.
  Yabusaki Y;
   Hayashi K,
   (HAYA/) HAYASHI K.
(SUMO ) SUMITOMO CHEM CO LTD.
   30-JUL-1993;
  21-JUL-1993;
20-JUL-1993;
  20-JUL-1994;
  22-MAR-1995
  variation
  Homo sapiens.
  Human auxillary cytochrome P450 species 2A6 variant 1 coding region.
  Human cytochrome P450; amplification; PCR; primer; expression vector; yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
  14-NOV-1995 (first entry)
  AAQ87722 standard; cDNA; 1485 BP
   carcinogen; mutagen; liver metabolism; ds.
  AAQ87722;
   420 gggcaagcgaggcatcgaggagcgcatccaggag 453
  360 cggggagcgccaagcagctccggcgcttctccatcgccaccctgcgggacttcggggt 419
   66 999cgt999gggggacaggaattgaagcggaag 99
   6 cgctgggcaggcggggcagctcctgggggtcctcgggagaccactgcgctccacggttgaggt 65
   Kaneko H, Komai K,
  Conservative
   93JP-0180246.
93JP-0201120.
93JP-0208279.
  94EP-0111298
   /*tag= a
/note= "G to A change in variant 1 changes amino
acid from Arg to Lys"
  Location/Qualifiers 1427
   /*tag=
  0; Mismatches
   Nakatsuka I,
  39;
   Sakaki T;
  Indels
  0; Gaps
  0;
```

```
밁
                                  QΥ
   В
   SSXSS
  Matches
  Query Match
Best Local :
   Sequence 1485 BP; 328 A; 430 C; 412 G; 315 T; 0 other;
   converted into a carcinogenic or mutagenic form through metabolism in the
  liver.
420 gggcaagcgaggcatcgaggagcgcatccaggag 453
   360 cggggagcgccaagcagctccggcgcttctccatcgccaccctgcgggacttcggggt 419
                   66 gggcgtggggggggggacaggaattgaagcggaag 99
   6 cgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgttgaggt 65
  55;
   h 25.3%;
Similarity 58.5%;
55; Conservative
   0; Mismatches
   Score 31.6; DB 16; Length 1485; Pred. No. 7;
   39; Indels
   0;
   Gaps
   0;
```

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